

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 11, 2004, 18:40:43 ; Search time 8349 Seconds

(without alignments)
7833.055 Million cell updates/sec

Title: US-10-690-617-1

Perfect score: 2190

Sequence: 1 cgccgcgggtgagctcgg.....ctctgtctattcagacgct 2190

Scoring table: IDENTITY NUC

Gapop 10_0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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1: em_estba:*

2: em_esthum:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_htc:*

9: gb_est1:*

10: gb_est2:*

11: gb_htc:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: em_gss_hum:*

18: em_gss_inv:*

19: em_gss_pin:*

20: em_gss_vrt:*

21: em_gss_fun:*

22: em_gss_mam:*

23: em_gss_mus:*

24: em_gss_pro:*

25: em_gss_rod:*

26: em_gss_phg:*

27: em_gss_vrl:*

28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1511.6	69.0	1518	29	AY416154 Homo sapi
2	1225.6	56.0	1518	29	AY416156 Mus muscu
3	1059.8	48.4	1445	29	AY416155 Pan trogl
4	940	42.9	1201	9	AL539375 AL539375

5	928.2	42.4	1034	13	EX401350
6	912.4	41.7	1201	13	EX395129
7	844.2	38.5	972	13	EX459685
8	822.4	37.6	1096	12	BM805189
9	790.8	36.1	2199	11	BC011401
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11	742.4	33.9	880	12	BG705317
12	732	33.4	910	13	BQ32168
13	729.8	33.3	1066	13	BQ277875
14	727	33.2	786	12	BI819446
15	702.4	32.1	896	13	EX328136
16	692.6	31.6	893	12	BG396486
17	668.6	30.5	784	13	BQ571613
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25	556	25.4	1127	13	BU902211
26	529.2	24.2	648	12	BG294573
27	502.6	22.9	589	13	BU671280
28	462.8	21.1	515	12	BM087446
29	445.6	20.3	672	13	BY735290
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32	429.8	19.6	841	13	BU115704
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34	417	19.0	496	14	CB712914
35	415.6	19.0	589	14	CA751670
36	407.4	18.6	703	28	AQ629789
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ALIGNMENTS

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LOCUS	AY416154	Homo sapiens CMKK1 gene, VIRTUAL TRANSCRIPT, partial sequence,			
DEFINITION	AY416154	genomic survey sequence.			
ACCESSION	AY416154.1	GI:39772114			
VERSION	AY416154.1	GSS.			
KEYWORDS	AY416154.1	Homo sapiens (human)			
SOURCE	AY416154.1	Homo sapiens			
ORGANISM	AY416154.1	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
REFERENCE	AY416154.1	1 (bases 1 to 1518)			
AUTHORS	AY416154.1	Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferrier, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.			
TITLE	AY416154.1	Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios			
JOURNAL	AY416154.1	Science 302 (5652), 1960-1963 (2003)			
PUBMED	AY416154.1	14671302			
REFERENCE	AY416154.1	2 (bases 1 to 1518)			
AUTHORS	AY416154.1	Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferrier, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.			
TITLE	AY416154.1	Direct Submission			

JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
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/db_xref="taxon:9606"
gene <1..>1518
/gene="CAMKK1"
/locus_tag="HCM5796"
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Best local Similarity 99.7%; Pred. No. 5.2e-290;
Matches 1514; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 173 ATGGAGGGGGTCCAGCTGTCTGCTGCCAGGATCCTCGGCAGAGCTGTTAGAACGGGTG 232
DB 1 ATGGAGGGGGTCCAGCTGTCTGCTGCCAGGATCCTCGGCAGAGCTGTTAGAACGGGTG 60
QY 233 GCAGCCATCGATGTGACTCACTTGGAGAGGAGAGATGTTGCCAGAGCCCTACTAGAAAC 292
DB 61 GCAGCCATCGATGTGACTCACTTGGAGAGGAGAGATGTTGCCAGAGCCCTACTAGAAAC 120
QY 293 GGTGTGACCCGCCACACAGGGCCAGAGCTGCTCTGTGATCCCTGGCAGTACTTCAAGA 352
DB 121 GGTGTGACCCGCCACACAGGGCCAGAGCTGCTCTGTGATCCCTGGCAGTACTTCAAGA 180
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QY 1673 GACGAGCTGCATCCTGA 1690
DB 1501 GACGAGCTGCATCCTGA 1518
RESULT 2
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LOCUS 1518 bp DNA linear GSS 17-DEC-2003
DEFINITION Mus musculus CAMKK1 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION AY416156
VERSION AY416156.1 GI:39772116
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1518)
AUTHORS Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civallo,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sainsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 1518)
AUTHORS Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,

Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D., and Cargill, M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment.

FEATURES
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Best Local Similarity 87.4%; Pred. No. 4.3e-233;
Matches 1327; Conservative 0; Mismatches 191; Indels 0; Gaps 0;
QY 173 ATGGAGGGGGTCCAGCTGTCTGCTCCAGGATCTCGGGCAGAGCTGTGAACGGGTG 232
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DB 61 GGGCCATCAATGTGGCCCACTTGGAGAGCAGATGAGGGTCCAGAGCCTGCCAGGAT 120
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RESULT 3

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LOCUS
DEFINITION
Pan troglodytes CAMKK1 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION
AY416155
VERSION
AY416155.1 GI:39772115
KEYWORDS
GSS.
SOURCE
Pan troglodytes (chimpanzee)
ORGANISM
Pan troglodytes
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE
1 (bases 1 to 1445)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
TITLE
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios

JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 146711302
REFERENCE 2 (bases 1 to 1445)
AUTHORS Clark,A.G., Glatowski,S., Nielson,R., Thomas,P., Kejarimal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferrira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
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Best Local Similarity 73.6%; Pred. No. 4.1e-200;
Matches 1064; Conservative 0; Mismatches 381; Indels 0; Gaps 0;
Qy 173 ATGAGGGGGTCCAGCTGTCTGCGCAGGATCCTGGGCAGAGCTGTAGACGGGTG 232
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Qy 1 ATGAGGGGGTCCAGCTGTCTGCGCAGGATCCTGGGCAGGCTGTAGACGGGTG 60
Db |||||
Qy 233 GCAGCCATCATGTGACTCACTTGGAGGAGCAGATGGTGGCCAGAGCCCTACTAGAAC 292
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Qy 293 GGTGTGAGCCGCCACCAACCGGCCAGAGCTGCTGTGATCCCTGGAGTACTTCAAGA 352
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Qy 181 CTGCTCCAGCCCGGCTAGCTCTCAGCCAGGAGCTTTCCCTACAGGAGCGGCCAGCA 240
Qy 413 GGAAGCTATCTGAGGCGCAGGCTGCGCTTATGCCACGGGCTTGCAGCACATCTCC 472
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Qy 1373 CCAGACATCAAGTTGACCCCTTGGGTGACCAAGAACCGGGAGGAGCCCTTCTTTCGAG 1432
Db CCAGACATCAAGTTGACCCCTTGGGTGACCAAGAACCGGGAGGAGCCCTTCTTTCGAG 1260
Qy 1433 GAGGAGCACTGCAGCGTGTGGAGTGCAGAGGGGAGGTTAAGAACTCAGTCAGGCTC 1492
Db GAGGAGCACTGCAGCGTGTGGAGTGCAGAGGGGAGGTTAAGAACTCAGTCAGGCTC 1320
Qy 1493 ATCCCAAGCTGGACCAAGTGTGCTGTAAGTCCATGCTGAGGAAGCGTCTTCTTGGG 1552
Db ATCCCAAGTGGACCAAGTGTGCTGTAAGTCCATGCTGAGGAAGCGTCTTCTTGGG 1380
Qy 1553 AACCGTTTTCAGCCCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1612
Db AACCGTTTTCAGCCCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1440
Qy 1613 CTGGT 1617
Db CTGGT 1445
RESULT 4
AL539375
LOCUS AL539375 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone
DEFINITION CS0DF033Y017 5-PRIME, mRNA sequence.
ACCESSION AL539375
VERSION AL539375.2 GI:31263943
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1201)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On Feb 15, 2001 this sequence version replaced gi:12868532.
Contact: Genoscope
Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France
 Email: segre@genoscope.cns.fr, Web : www.genoscope.cns.fr
 Library was constructed by Life Technologies, a division of
 Invitrogen. This sequence belongs to sequence cluster 8786.r For
 more information about this cluster, see
 http://www.genoscope.cns.fr/
 cgi-bin/cluster.cgi?seq=CS0DF033AH09QPl&cluster=8786.r. Contact :
 Feng Liang Email : fliang@lifetech.com URL :
 http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
 Faraday Avenue Genoscope sequence ID : CS0DF033AH09QPl.
 Location/Qualifiers
 1. .1201
 /organism="Homo sapiens"
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 /note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
 was primed with a NotI-oligo(dT) primer. Five prime end
 enriched, double-strand cDNA was digested with Not I and
 cloned into the Not I and EcoRV sites of the pCMVSPORT 6
 vector. Library was not normalized."

FEATURES source

ORIGIN

Query Match 42.9%; Score 940; DB 9; Length 1201;
 Best Local Similarity 97.2%; Pred. No. 2.6e-176;
 Matches 1005; Conservative 5; Mismatches 16; Indels 8; Gaps 5;

QY 178 GGGGGGTCTAGTGTCTGTCAGAGATCTCTCGGCAGAGCTGGTAGAACGGGTGGCAGC 237
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 QY 238 CATCATGTGACTACTTGGAGAGGCGAGATGCTGCGCCAGAGCCCTACTAGAAACGGTGT 297
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 QY 358 CCCAGCCGGCTAGCTCTCAGCAGGAGGTTTCCCTACAGAGCGGCCAGCAGGAAG 417
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 QY 1077 GGAAGGAGCTCAGCTGTCAGGAGCGGGGAGCCAGCAGCTTATGCCCCCGAGGCA 1136
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 QY 1197 CTTTGTACTGCTTT 1210
 Db 1078 CTTTGTACTGHTTK 1091

RESULT 5
 BX401350
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

BX401350 1034 bp mRNA linear EST 13-MAY-2003
 CDNA clone CS0DK012YG22 5-PRIME, mRNA sequence.
 BX401350
 BX401350.1 GI:30630361
 EST.
 Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1. (bases 1 to 1034)
 Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
 Full-length cDNA libraries and normalization
 Unpublished (2001)
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: segre@genoscope.cns.fr, Web : www.genoscope.cns.fr
 Library was constructed by Life Technologies, a division of
 Invitrogen. This sequence belongs to sequence cluster 8786.r For
 more information about this cluster, see
 http://www.genoscope.cns.fr/
 cgi-bin/cluster.cgi?seq=CS0DK012BD11QPl&cluster=8786.r. Contact :
 Feng Liang Email : fliang@lifetech.com URL :
 http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
 Faraday Avenue Genoscope sequence ID : CS0DK012BD11QPl.
 Location/Qualifiers
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 /mol_type="mRNA"
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 /note="1st strand cDNA was primed with a NotI-oligo(dT)
 primer. Five prime end enriched, double-strand cDNA was
 digested with Not I and cloned into the Not I and EcoRV
 sites of the pCMVSPORT 6 vector. Library was normalized."

FEATURES
 source

ORIGIN

Abramson, R.D., Mullaby, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahy, J., Helton, E., Kettelman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krywinski, M.I., Skalska, U., Smalish, D.E., Schnerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

22388257

12477932

2 (bases 1 to 2199)

Strausberg, R.

Direct Submission

Submitted (25-JUL-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contact: MGC help desk

Email: cgabbs-r@mail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center

Center code: BCM-HGSC

Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>

Contact: ang@bcm.tmc.edu

Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Lounseged, H., Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati, A.N., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Series: IRAK Plate: 13 Row: n Column: 11

This clone has the following problem: retained intron.

FEATURES

source

1. .2199

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/db_xref="taxon:9606"

/clone="IMAGE:3873973"

/tissue_type="Eye, retinoblastoma"

/clone_lib="NIH_MGC_67"

/lab_host="DH10B"

/note="Vector: pCMV-SPORT6"

ORIGIN

Query Match 36.1%; Score 790.8; DB 11; Length 2199;

Best Local Similarity 99.7%; Pred. No. 1.7e-146;

Matches 792; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 1 GTGACCAAGACGGGAGGAGCCCTTCTTCGGAGGAGGACATCTGCAGCGTGGTGAG 60

QY 1457 GTGACAGAGGGGAGGTTAAGAACTCAGTCAGGCTCATCCAGCTGGACACCGGTGATC 1516

Db 61 GTGACAGAGGAGGAGGTTAAGAACTCAGTCAGGCTCATCCAGCTGGACACCGGTGATC 120

QY 1517 CTGGTGAAGTCATCTGAGGAGCGTCTCTTTGGAAACCGTTTTCAGCCCGACGCG 1576

Db 121 CTGGTGAAGTCATCTGAGGAGCGTCTCTTTGGAAACCGTTTTCAGCCCGACGCG 180

QY 1577 AGGGAGAGCGATCCATGTCTGCTCCAGGAACCTACTGCTGAAGAAAGGTTTGTGAA 1636

Db 181 AGGGAGAGCGATCCATGTCTGCTCCAGGAACCTACTGCTGAAGAAAGGTTTGTGAA 240

QY 1637 GGGGGCAAGAGCCCGAGAGCTCCCGCGCTCCAGGAAGACGAGGCTGCATCTTGAGCCCT 1696

Db 241 GGGGGCAAGAGCCCGAGAGCTCCCGCGCTCCAGGAAGACGAGGCTGCATCTTGAGCCCT 300

QY 1697 GCATGCACCCAGGGCCACCCGCGACACACTCATCCCGCGCTCCAGAGGCCACCCCTC 1756

Db 301 GCATGCACCCAGGGCCACCCGCGACACACTCATCCCGCGCTCCAGAGGCCACCCCTC 360

QY 1757 ATGCAACAGCCGCCCGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1816

Db 361 ATGCAACAGCCGCCCGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 420

QY 1817 CCATCGTCTGATGATGATCTCCACGACGACGCTCCAGGACAGACTGGAATGTATGTCA 1876

Db 421 CCATCGTCTGATGATGATCTCCACGACGACGCTCCAGGACAGACTGGAATGTATGTCA 480

QY 1877 TTTGGGCTCTTGGGGCAGGGCTCCACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1936

Db 481 TTTGGGCTCTTGGGGCAGGGCTCCACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 540

QY 1937 CTTGACCCATCTTGTGGGAAAACCGGGTCCCATGGAGGCTCAGAAATGCCACCCGGCTG 1996

Db 541 CTTGACCCATCTTGTGGGAAAACCGGGTCCCATGGAGGCTCAGAAATGCCACCCGGCTG 600

QY 1997 GTTGGCATGGCTTGGGGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2056

Db 601 GTTGGCATGGCTTGGGGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 660

QY 2057 GCTTACCAACAGGAGAGACCTCCCGCTGGGGCGGGGAGGAGGAGGAGGAGGAGGAGGAG 2116

Db 661 GCTTACCAACAGGAGAGACCTCCCGCTGGGGCGGGGAGGAGGAGGAGGAGGAGGAGGAG 720

QY 2117 GGCATATGTTGAGAGGGGGGTACCTGCGCCACCTTGGGGTGGTGACACAGAGCTCTTG 2176

Db 721 GGCATATGTTGAGAGGGGGGTACCTGCGCCACCTTGGGGTGGTGACACAGAGCTCTTG 780

QY 2177 TCTATTGACAGCGT 2190

Db 781 TCTATTGACAGCGT 794

RESULT 10

BU552890

LOCUS

DEFINITION AGENCOURT 10373297 NIH_MGC 109 Homo sapiens cDNA clone

IMAGE:6576737 5', mRNA sequence.

ACCESSION BU552890

VERSION BU552890.1 GI:22903162

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 939)

NIH-MGC <http://mgc.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgabbs-r@mail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Rubin Laboratory

DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Plate: LLCM2775 row: 1 column: 17

High quality sequence stop: 659.

Location/Qualifiers

1. .939

/organism="Homo sapiens"

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/db_xref="taxon:9606"

FEATURES

source

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Best Local Similarity	97.2%;	Pred. No. 7.1e-146;		
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QY	857	GTGTTTGACCTCTCGAGAAAGGGGCCCGT	CATGGAAAGTGCCTGTGACAAAGCCCTTCTCG	916
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QY	917	GAGAGCAAGCTCGCCTTACCTTCGCGGACGT	CATCCTGGGCTTCGAGTACTTTGCACATGC	976
Db	98	GAGAGCAAGCTCGCCTTACCTTCGCGGACGT	CATCCTGGGCTTCGAGTACTTTGCACATGC	157
QY	977	CAGAAATGTCACAGGGGACATCAAGCCATCCAA	CCTGCTCTCTGCGGGATGATGGCAC	1036
Db	158	CAGAAATGTCACAGGGGACATCAAGCCATCCAA	CCTGCTCTCTGCGGGATGATGGCAC	217
QY	1037	GTGAAGATCGCCGACCTTTGGCGTTCAGCAAC	CCAGTTTTGAGGGGAAACGACGCTCAGCTGTCC	1096
Db	218	GTGAAGATCGCCGACCTTTGGCGTTCAGCAAC	CCAGTTTTGAGGGGAAACGACGCTCAGCTGTCC	277
QY	1097	AGCACGGCGGGAACCCGACGATTCATGCCCC	CCGAGGCCATTTTCTGATTCGCGCCAGAGC	1156
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QY	1277	CCCGTGGTGTTCCTCGAGGACGAGAAATCAG	CGAGGAGCTCAAGGACCTGATCTCTGAAG	1336
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QY	1337	ATGTTAGACAAGAATCCCGAGACGAGAAAT	TGGGGTGCACAGCATCAAGTTGCAACCTTGG	1396
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QY	1397	GTGACCAAGAAACGGGGAGGAGCCCTTCCTT	TCGAGGAGGAGCACTGCAGCGTGTGGAG	1456
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QY	1457	GTCAAGAGGGGAGGTTTAAGAACTCAGTCAG	GCTCATCCACAGCTGGACCAAGTGTATC	1516
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QY	498	TGAGTCCCAACACGTCGGGCATCTCAGATGCGAGGAGCTGCGTGCAGCTGAACCACTACA	557
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QY	558	AGCTGCGAGTGAATTTGGCAGGGTGCCTACGGTGTGTGGTGGCTGCGCTACAGCAAA	617
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QY	738	AGCTGTCGCCCTGGAGCGGGTACACAGAGATTGCCATCTCTGAAGAGCTGGACGAG	797
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QY	978	AGAA-GATCGTCCACA-GGGACATCAAGCCATCCAACTGCTCTCGGGGATGATGGGCA	1035
Db	780	AGNAGGATGTCACAGGGGACCTCAGCCATGCACTGCTCTGGGGGATGATGGCC	839
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Db	840	GGAAGCATCGGCAAGTAGCGGT 863	
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DEFINITION			
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BQ932168			
VERSION			
BQ932168.1 GI:22347199			
KEYWORDS			
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SOURCE			
Homo sapiens (human)			
ORGANISM			
Homo sapiens			
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
1 (bases 1 to 910)			
NIH-MGC http://mgi.nci.nih.gov/.			
AUTHORS			
National Institutes of Health, Mammalian Gene Collection (MGC)			
TITLE			
Unpublished (1999)			
COMMENT			
Contact: Robert Strausberg, Ph.D.			
Email: cga@rsf@mail.nih.gov			
Tissue Procurement: Dr. James R. Lupski			
CDNA Library Preparation: Life Technologies, Inc.			
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)			
DNA Sequencing by: Agencourt Bioscience Corporation			
Clone distribution: MGC clone distribution information can be			
found through the I.M.A.G.E. Consortium/LLNL at:			
http://image.llnl.gov			
Plate: LLAMI3606 row: e column: 19			
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Directionally cloned using the following adaptors:			
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5'-GACTAGTTCTAGATCGGAGCGCGCCCT(15)-3'. Size selected >			
1 kb for average insert length 1.87 kb. This is a primary			
library, non-amplified. Library constructed by Life			
Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor			
College of Medicine) and is available through Life			
Technologies."			
ORIGIN			
Query Match 33.4%; Score 732; DB 13; Length 910;			
Best Local Similarity 94.4%; Pred. NO. 5.6e-135;			
Matches 849; Conservative 0; Mismatches 31; Indels 19; Gaps 8;			
QY	272	GGCCAGAGCGCTACTAGAAACGGTGTGACCCCGCCACCGGCGCCAGAGCTGCTCTGTG	331
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QY	332	ATCCCTGGCAGTACTTCAAGACTGTCTCCAGCGCGGCTAGCTCTCAGCAGGAAGCTT	391
Db	61	ATCCCTGGCAGTACTTCAAGACTGTCTCCAGCGCGGCTAGCTCTCAGCAGGAAGCTT	120
QY	392	TCCTTACAGAGCGGCGCAGAGAACTATCTGAGGCGGAGCTGGGCTTATGCCAG	451
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QY	452	GGGCTGCGCAGCCACATCTCCCGGGGCTGGGAGGCGCCACCATCAGTCCCACAC	511
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QY	512	GTGGCCATCTCAGATGCGAGGAGCTCGTGCAGCTCAACAGTACAAGCTGCAGAGTAG	571
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QY	572	ATTGGCAAGGTCCTACGGTGTGAGGCTGGGCTTACAAAGAAAGTGAAGACAGAC	631
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QY	632	TATGCAATGAAAGTCTCTTCCAAAAGAAAGTACTGAAGCAGTATGGCTTTCCACGTCG	691
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QY	752	GAGCGGCTGTACAGGAGATTGGCATCTCTGAAGAGCTGGACCACTGAATGTGTCATA	811
Db	481	GAGCGGCTGTACAGGAGATTGGCATCTCTGAAGAGCTGGACCACTGAATGTGTCATA	540
QY	812	CTGATCGAGTCTCTGATGATCAGCTGAGGAGCACTCTATTGTGTTTGTACCTCTCTG	871
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QY	872	AGAAAGGGGCGCGCTCATGGAAGTGGCCCTGTGACAGCCCTTCTCGGAGGAGC-AACTCG	930
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QY	931	CCTCTACCTGCGGAGCTCATCTCTGGGCTCTGAGTACTTGTGACCTGCGCAGAGATCTCCA	990

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RESULT 13
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LOCUS AGENCOURT 7048118 NIH_MGC_109 Homo sapiens cDNA clone IMAGE:5804754
5', mRNA sequence.
ACCESSION BQ277875
VERSION BQ277875.1 GI:20488083
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1066)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: csaapb-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LICM2042 row: n column: 19
High quality sequence stop: 626.
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/clone_lib="NIH_MGC_109"
/note="Organ: ovary; Vector: pOTB7; Site: 1: EcoRI; Site: 2:
XhoI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGACGACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."
ORIGIN
Query Match 33.3%; Score 729.8; DB 13; Length 1066;
Best Local Similarity 89.7%; Pred. No. 1.7e-134;
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ACCESSION BI819446
VERSION BI819446.1 GI:15930996
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 786)
 NIH-MGC <http://mgc.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgabs-r@mail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
<http://image.lnl.gov>
 Plate: L14M11436 row: d column: 09
 High quality sequence stop: 786.
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 source anonymous pool of 6 male brains, age range 23-27; 1
 male lung, age 27; and 1 male testis, age 69. Library is
 oligo-dT primed and directionally cloned (EcoRV site is
 destroyed upon cloning). Average insert size 1.8 kb,
 insert size range 1-3 kb. Library is normalized and
 enriched for full-length clones and was constructed by C.
 Gruber (Invitrogen). Research Genetics tracking code
 021. Note: this is a NIH_MGC Library."

RESULT 15
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 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

REFERENCE
 AUTHORS
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 JOURNAL
 COMMENT

FEATURES
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Query Match
 Best Local Similarity 33.2%; Score 727; DB 12; Length 786;
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QY 91 CGCCCGCCGCGGACGACCTGTGCGCCGCGCCAGGTTCCCAACAGGCTACGCGAG 150
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 DB 181 TGGCCCGAGAGCTTACTAGAAAAGTGTGACACCCCGCCAGGCGGCGAGAGTGCCTCTGT 240

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QY 391 TTCCCTACAGGAGCGCGAGGAGCTATCTGAGGGCGAGGCTTGGGCGCTTATGCCAC 450
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QY 451 GGGGCGCTGCAGCCACATCTCCCGCGGCTGGCGAGGCGCCACCATCGAGTCCACCA 510
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RESULT 15
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 ORGANISM

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 TITLE
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FEATURES
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 Best Local Similarity 32.1%; Score 702.4; DB 13; Length 896;
 Matches 787; Conservative 0; Mismatches 61; Indels 8; Gaps 4;

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Search completed: July 12, 2004, 01:17:37
Job time : 8355 secs

Db 361 AGCCGCGCTAGCCTCTCAGCCAGAAAGCTTTCCCTACAGAGCGGCCAGCAGAGCTA 420
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RESULT 2

US-10-135-689-1
; Sequence 1, Application US/10135689
; Patent No. 6670162
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL000904DIV
; CURRENT APPLICATION NUMBER: US/10/135,689
; CURRENT FILING DATE: 2002-05-01
; PRIOR APPLICATION NUMBER: 60/247,031
; PRIOR FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: 09/729,995
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2190
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-135-689-1

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QY	241	CGATGTGACTCACTTGGAGGAGCAGATGGTGGCCAGAGCCTACTAGAAAAGGTGTGA	300	QY	1261	GAAATCAAGATGAGCCGCTGGTGTCTTCTGAGGAGCCAGAAATCAGCGAGAGCTCAA	1320		
DB	241	CGATGTGACTCACTTGGAGGAGCAGATGGTGGCCAGAGCCTACTAGAAAAGGTGTGA	300	DB	1261	GAAATCAAGATGAGCCGCTGGTGTCTTCTGAGGAGCCAGAAATCAGCGAGAGCTCAA	1320		
QY	301	CCCCCAACACGGGCGAGAGTGCCTGTGTATTCCTGGCAGTACTTCAAGACTGTCTCC	360	QY	1321	GGACCTGATCTTGAAGATGTTAGACAAGATCCCAGAGCAGAAATTTGGGTGCCACAT	1380		
DB	301	CCCCCAACACGGGCGAGAGTGCCTGTGTATTCCTGGCAGTACTTCAAGACTGTCTCC	360	DB	1321	GGACCTGATCTTGAAGATGTTAGACAAGATCCCAGAGCAGAAATTTGGGTGCCACAT	1380		
QY	361	AGCCGGGCTAGCCTCTCAGCAGAGAACTTTCCCTACAGAGCGGCGAGCAGGAAGCTA	420	QY	1381	CAAGTTGCACCTTGGGTGACCAAGAACGGGAGGAGCCCTTCTTCGGAGGAGGAGCA	1440		
DB	361	AGCCGGGCTAGCCTCTCAGCAGAGAACTTTCCCTACAGAGCGGCGAGCAGGAAGCTA	420	DB	1381	CAAGTTGCACCTTGGGTGACCAAGAACGGGAGGAGCCCTTCTTCGGAGGAGGAGCA	1440		
QY	421	TCTGAGGCGCAGGCTGGGCTTATGCCACGGGGCTTCGACGACATCTCCCGCGGC	480	QY	1441	CTGACAGCTGGTGGAGGTGACAGAGGGGAGGTTAAGAACTCAGTCAGGCTCATCCCCAG	1500		
DB	421	TCTGAGGCGCAGGCTGGGCTTATGCCACGGGGCTTCGACGACATCTCCCGCGGC	480	DB	1441	CTGACAGCTGGTGGAGGTGACAGAGGGGAGGTTAAGAACTCAGTCAGGCTCATCCCCAG	1500		
QY	481	CTGGCGAGGCCACCATCGAGTCCCAACAGTGGCCATCTCAGATGACAGGACTGCGT	540	QY	1501	CTGGACCAAGGTTCCTGGTCAAGTCCATGCTCAGGAAGCGTTCCTTTGGGAAACCGCTT	1560		
DB	481	CTGGCGAGGCCACCATCGAGTCCCAACAGTGGCCATCTCAGATGACAGGACTGCGT	540	DB	1501	CTGGACCAAGGTTCCTGGTCAAGTCCATGCTCAGGAAGCGTTCCTTTGGGAAACCGCTT	1560		
QY	541	GCAGCTGAACCAAGTGAAGACAGACATATGCAATGAAAGTCTTTCAAAAGAA	600	QY	1561	TCAGCCCCAGGCAACGGAGGAAGCGATCATCTGTCTCCAGGAACCTACTGTGTGAA	1620		
DB	541	GCAGCTGAACCAAGTGAAGACAGACATATGCAATGAAAGTCTTTCAAAAGAA	600	DB	1561	TCAGCCCCAGGCAACGGAGGAAGCGATCATCTGTCTCCAGGAACCTACTGTGTGAA	1620		
QY	601	GCTGGCCTACAAAGTGAAGACAGACATATGCAATGAAAGTCTTTCAAAAGAA	660	QY	1621	AGAAGGTTTGGTGAAGGGGCAAGAGCCAGAGTCCCCGGCGTCCAGGAAGACGAGGC	1680		
DB	601	GCTGGCCTACAAAGTGAAGACAGACATATGCAATGAAAGTCTTTCAAAAGAA	660	DB	1621	AGAAGGTTTGGTGAAGGGGCAAGAGCCAGAGTCCCCGGCGTCCAGGAAGACGAGGC	1680		
QY	661	GTACTGAAGAGTATGGCTTTCCAGTGGCCCTCCCGAGAGGTTCCAGGCTGCCA	720	QY	1681	TGCATCTGAGCCCTGTGATGACCCAGGGCCACCCGAGGCACTCATCCCGCGCTC	1740		
DB	661	GTACTGAAGAGTATGGCTTTCCAGTGGCCCTCCCGAGAGGTTCCAGGCTGCCA	720	DB	1681	TGCATCTGAGCCCTGTGATGACCCAGGGCCACCCGAGGCACTCATCCCGCGCTC	1740		
QY	721	GGGAGACAGCCAGCAGCTGCTGCCCTGGAGCGGTGTACAGGAGATTCCTT	780	QY	1741	CAGAGGCCACCTCTCATGCAACAGCCGCCCGCAGGCGAGGGGCTGGGAGCTGCAGCC	1800		
DB	721	GGGAGACAGCCAGCAGCTGCTGCCCTGGAGCGGTGTACAGGAGATTCCTT	780	DB	1741	CAGAGGCCACCTCTCATGCAACAGCCGCCCGCAGGCGAGGGGCTGGGAGCTGCAGCC	1800		
QY	781	GAAAGAGCTGGACCAAGTGAATGTGTCAAACTGATCGAGGTCTTGGATGACCCAGCTGA	840	QY	1801	CACTCCCCCGCTCCCGCATCGTGTGATGACCTTCACGCAACGACGCTCCAGGAGCAG	1860		
DB	781	GAAAGAGCTGGACCAAGTGAATGTGTCAAACTGATCGAGGTCTTGGATGACCCAGCTGA	840	DB	1801	CACTCCCCCGCTCCCGCATCGTGTGATGACCTTCACGCAACGACGCTCCAGGAGCAG	1860		
QY	841	GGACAACTTATTTGGTGTGACTCTCTAGAAAAGGGCCCGTATGGAAGTGCCTG	900	QY	1861	ACTGGAATGTATGTATTTGGGTCTTTGGGGCAGAGGCTCCCAAGAGGCCATCTCTCTCT	1920		
DB	841	GGACAACTTATTTGGTGTGACTCTCTAGAAAAGGGCCCGTATGGAAGTGCCTG	900	DB	1861	ACTGGAATGTATGTATTTGGGTCTTTGGGGCAGAGGCTCCCAAGAGGCCATCTCTCTCT	1920		
QY	901	TGACAGCCCTTCTCGGAGAGCAAGCTCGCCTCTACCTGCGGAGCTCATCTGGGCT	960	QY	1921	TCTTGGCCCTCTTGGCCCTGACCCATTTCTGTGGGGAACCGGGTCCCATGGAGCCTCAG	1980		
DB	901	TGACAGCCCTTCTCGGAGAGCAAGCTCGCCTCTACCTGCGGAGCTCATCTGGGCT	960	DB	1921	TCTTGGCCCTCTTGGCCCTGACCCATTTCTGTGGGGAACCGGGTCCCATGGAGCCTCAG	1980		
QY	961	CGAGTACTTGCATGCCAAGAGATGTTCCACAGGAGCATCAAGCCATCCAACTGTCTCT	1020	QY	1981	AAATGCACCCCGCTGTTGGCATGSCCTGGGCGAGGAGGAGGAGGAGGAGGAGGAGGAG	2040		
DB	961	CGAGTACTTGCATGCCAAGAGATGTTCCACAGGAGCATCAAGCCATCCAACTGTCTCT	1020	DB	1981	AAATGCACCCCGCTGTTGGCATGSCCTGGGCGAGGAGGAGGAGGAGGAGGAGGAGGAG	2040		

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Db 2101 TGGCTCAGCTGCCACAGCATATGGTGGAGAGGGGGGTACCTGCCACCTTGGGGTGGT 2160
|||||
Qy 2161 GGCACCAAGAGCTTTGTCTATTACAGCGCT 2190
|||||
Db 2161 GGCACCAAGAGCTTTGTCTATTACAGCGCT 2190
|||||
RESULT 3
US-09-729-995-3
; Sequence 3, Application US/09729995
; Patent No. 6426206
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL000904
; CURRENT APPLICATION NUMBER: US/09/729,995
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 29629
; TYPE: DNA
; ORGANISM: Human
US-09-729-995-3

Query Match 25.6%; Score 561.4; DB 4; Length 29629;
Best Local Similarity 96.4%; Pred. No. 1.6e-122;
Matches 585; Conservative 0; Mismatches 21; Indels 1; Gaps 1;
Qy 1585 GCGATCATGTCCTCCACAGAAACCTACTGTTGTAAGAGGGTTTGGTGAAGGGGCAA 1644
Db 26526 GAGGTCCCTCTGTCCCTGTCTCCCTGAACAGGAAAGAGGGTTTGGTGAAGGGGCAA 26585
Qy 1645 GAGCCACAGAGCTCCCGCGCTCCAGGAAGACAGAGCTGCATCTCGAGCCCTCGCATGCAC 1704
Db 26586 GAGCCACAGAGCTCCCGCGCTCCAGGAAGACAGAGCTGCATCTCGAGCCCTCGCATGCAC 26645
Qy 1705 CAGGGGCACCCCGCAGACACTCATCCCGGCTCCAGAGGCCA-CCCTCATGCAAC 1763
Db 26646 CAGGGGCACCCCGCAGACACTCATCCCGGCTCCAGAGGCCA-CCCTCATGCAAC 26705
Qy 1764 AGCCGCCCCCGCAGCGAGGGGCTGGGGACTGACAGCCCACTCCCGCCCTCCCGCATCG 1823
Db 26706 AGCCGCCCCCGCAGCGAGGGGCTGGGGACTGACAGCCCACTCCCGCCCTCCCGCATCG 26765
Qy 1824 TGCTGCATGACCTCCACGACGACGCTCCAGGGACAGACTGGAAATGTATGTATTGGGG 1883
Db 26766 TGCTGCATGACCTCCACGACGACGCTCCAGGGACAGACTGGAAATGTATGTATTGGGG 26825
Qy 1884 TCTTGGGGGAGGGCTCCAGAGGCCATCTCTCTTCTTGGCCCTCTTGGCCTGACC 1943
Db 26826 TCTTGGGGGAGGGCTCCAGAGGCCATCTCTCTTCTTGGACCTCTTGGCCTGACC 26885
Qy 1944 CATTTCTGTGGGAAACCGGGTGCCTAGAGCTTCAGAAATGCCACCGGCTGTGGCA 2003
Db 26886 CATTTCTGTGGGAAACCGGGTGCCTAGAGCTTCAGAAATGCCACCGGCTGTGGCA 26945
Qy 2004 TGGCCTGGGGCAGGAGCAGAGGACAGAGACCAAGATGGCAGGTGGAGGCCAGGCTTACC 2063
Db 26946 TGGCCTGGGGCAGGAGCAGAGGACAGAGACCAAGATGGCAGGTGGAGGCCAGGCTTACC 27005
Qy 2064 ACAACGAAGAGACTTCCCGCTGGGGCCGGCAGGCTTGGCTCAGCTGCCACAGGCATAT 2123
Db 27006 ACAACGAAGAGACTTCCCGCTGGGGCCGGCAGGCTTGGCTCAGCTGCCACAGGCATAT 27065
Qy 2124 GGTGGAGAGGGGGTACCTCTGCCACCTTGGGGTGGTGGCACCAGAGCTCTTGTCTATTTC 2183
Db 27066 GGTGGAGAGGGGGTACCTCTGCCACCTTGGGGTGGTGGCACCAGAGCTCTTGTCTATTTC 27125
Qy 2184 AGACGCT 2190

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Db 27126 AGACGCT 27132
|||||
RESULT 4
US-10-135-689-3
; Sequence 3, Application US/10135689
; Patent No. 6670162
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL000904DIV
; CURRENT APPLICATION NUMBER: US/10/135,689
; PRIOR FILING DATE: 2002-05-01
; PRIOR APPLICATION NUMBER: 60/247,031
; PRIOR FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: 09/729,995
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 29629
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-135-689-3

Query Match 25.6%; Score 561.4; DB 4; Length 29629;
Best Local Similarity 96.4%; Pred. No. 1.6e-122;
Matches 585; Conservative 0; Mismatches 21; Indels 1; Gaps 1;
Qy 1585 GCGATCATGTCCTCCACAGAAACCTACTGTTGTAAGAGGGTTTGGTGAAGGGGCAA 1644
Db 26526 GAGGTCCCTCTGTCCCTGTCTCCCTGAACAGGAAAGAGGGTTTGGTGAAGGGGCAA 26585
Qy 1645 GAGCCACAGAGCTCCCGCGCTCCAGGAAGACAGAGCTGCATCTCGAGCCCTCGCATGCAC 1704
Db 26586 GAGCCACAGAGCTCCCGCGCTCCAGGAAGACAGAGCTGCATCTCGAGCCCTCGCATGCAC 26645
Qy 1705 CAGGGGCACCCCGCAGACACTCATCCCGGCTCCAGAGGCCA-CCCTCATGCAAC 1763
Db 26646 CAGGGGCACCCCGCAGACACTCATCCCGGCTCCAGAGGCCA-CCCTCATGCAAC 26705
Qy 1764 AGCCGCCCCCGCAGCGAGGGGCTGGGGACTGACAGCCCACTCCCGCCCTCCCGCATCG 1823
Db 26706 AGCCGCCCCCGCAGCGAGGGGCTGGGGACTGACAGCCCACTCCCGCCCTCCCGCATCG 26765
Qy 1824 TGCTGCATGACCTCCACGACGACGCTCCAGGGACAGACTGGAAATGTATGTATTGGGG 1883
Db 26766 TGCTGCATGACCTCCACGACGACGCTCCAGGGACAGACTGGAAATGTATGTATTGGGG 26825
Qy 1884 TCTTGGGGGAGGGCTCCAGAGGCCATCTCTCTTCTTGGCCCTCTTGGCCTGACC 1943
Db 26826 TCTTGGGGGAGGGCTCCAGAGGCCATCTCTCTTCTTGGACCTCTTGGCCTGACC 26885
Qy 1944 CATTTCTGTGGGAAACCGGGTGCCTAGAGCTTCAGAAATGCCACCGGCTGTGGCA 2003
Db 26886 CATTTCTGTGGGAAACCGGGTGCCTAGAGCTTCAGAAATGCCACCGGCTGTGGCA 26945
Qy 2004 TGGCCTGGGGCAGGAGCAGAGGACAGAGACCAAGATGGCAGGTGGAGGCCAGGCTTACC 2063
Db 26946 TGGCCTGGGGCAGGAGCAGAGGACAGAGACCAAGATGGCAGGTGGAGGCCAGGCTTACC 27005
Qy 2064 ACAACGAAGAGACTTCCCGCTGGGGCCGGCAGGCTTGGCTCAGCTGCCACAGGCATAT 2123
Db 27006 ACAACGAAGAGACTTCCCGCTGGGGCCGGCAGGCTTGGCTCAGCTGCCACAGGCATAT 27065
Qy 2124 GGTGGAGAGGGGGTACCTCTGCCACCTTGGGGTGGTGGCACCAGAGCTCTTGTCTATTTC 2183
Db 27066 GGTGGAGAGGGGGTACCTCTGCCACCTTGGGGTGGTGGCACCAGAGCTCTTGTCTATTTC 27125
Qy 2184 AGACGCT 2190

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Db      27126 AGAAGCT 27132      |||||
RESULT 5
US-09-016-434-1008
; Sequence 1008, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESS: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HERWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1008:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 288 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: BRAINOT04
; CLONE: 926034
; US-09-016-434-1008

Query Match      6.5%; Score 142.8; DB 4; Length 288;
Best Local Similarity 70.7%; Pred. No. 1.4e-24;
Matches 203; Conservative 0; Mismatches 83; Indels 1; Gaps 1;

QY      644 GTCTTTCCAAAAGAGTTACTGAAGCAGATATGGCTTTCCAGTCGCGCCCTCCCGGAGA 703
Db      1 GTGCTGTCCAAAAGAGCTGATCCGCGAGCGCGCTTTCCAGTCGCGCCCTCCCGGAGA 60

QY      704 GGGTCCAGCTGCCAGGAGGACGACGCCAGCAGCTGTCGCCCTCGAGCGGGGTGAC 763
Db      61 GGCACCCGGCGAGCTCTGTGAGGCTGCATCCAGCCAGGGGCCCCATTGAGCAGGGTGAC 120

QY      764 CAGGAGATTGCCATCTCTGAAGAGCTGGACACGTGAATGTGTCAAACTGATCGAGGTC 823
Db      121 CAGGAATTGGCCATCTCTCAGAAGCTGGACACCCCAATGTGTGAAGCTGTGGAGGTC 180

QY      824 CTGGATGACCCAGCTCAGGACCACTCTATTGTTGGTGTGTTGACCTCTCGAGAAAGGGGCCC 883
Db      181 CTGGATGACCCCAATGAGGACCATCTGTATCATGTGTGTA-ATGGTCAACCAAGGGGCC 239

QY      884 GTCATGGAAGTGCCTGTGTGACAGGCCCTTCTCGGAGGAGCAAGCTCG 930

Db      240 GTGATGAAGTGCCTCCACCCTTAACACCTTTTGAAGACCGGCGC 286
RESULT 6
US-09-016-434-809
; Sequence 809, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESS: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HERWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 809:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 236 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: BRAINOT03
; CLONE: 531037
; US-09-016-434-809

Query Match      4.5%; Score 99.4; DB 4; Length 236;
Best Local Similarity 71.8%; Pred. No. 2.1e-14;
Matches 155; Conservative 0; Mismatches 59; Indels 2; Gaps 2;

QY      875 AAGGGGCCCGTCATGGAAGTGCCC-TGTGACAAAGCCCTTCTCGGAGGAGCAAGCTGCGCT 933
Db      20 AAGGGGCCCGTGGATGGAAGTGCCCACTTTTAAACCACTCTCTGAAGACCAAGCCGTTT 79

QY      934 CTACCTGC--GGGACGTGATCTCTGGGCTCGAGTACTTGCATGCGCAGAGATCGTCCACA 992
Db      80 CTACTTCCAGGGATCTGATCAAGAGGATCGAGTACTTACACTACCAAGAGATCATCCACC 139

QY      993 GGGACATCAAGCCATCCAACTCTCCCTGGGGGATGATGGGCACTGGAAGATCGCCGACT 1052
Db      140 GTGACATCAAACTTTCAACCTCTGCTGCTCGGAGAGATGGGACATCAAGATCGCTGACT 199

QY      1053 TTGGGCTCAGCAACCAAGTTTGGAGGGGACACGCTC 1088
Db      200 TTGGTGTGAGCAATGAATTCAGGGGAGTGACGCGC 235
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RESULT 7
US-08-913-050A-2
; Sequence 2, Application US/08913050A
; Patent No. 5827726
; GENERAL INFORMATION:
; APPLICANT: NEZU, Jun-ichi
; TITLE OF INVENTION: DNA ENCODING PROTEIN KINASE
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
; STREET: 419 7th Street N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/913.050A
; FILING DATE: 05-SEP-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 57104/1995
; FILING DATE: 16-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP PCT/JP96/00660
; FILING DATE: 15-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: YUN, Allen C.
; REGISTRATION NUMBER: 37,971
; REFERENCE/DOCKET NUMBER: NEZU-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1302 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-913-050A-2
Query Match 4.1%; Score 90.4; DB 1; Length 1302;
Best Local Similarity 50.6%; Pred. No. 4.9e-12;
Matches 335; Conservative 0; Mismatches 306; Indels 21; Gaps 4;
Qy 758 GTGTACCAGGAGATTGCCATCCTGAAGAAGCTGGACCACTGTAATGTGGTCAAACTGATC 817
Db 283 GTGAAGAAGRAATTCACACTACTGAGGAGTTACGGCACAAAATGTCACTCAGCTGGT 342
Qy 818 GAGTCTCGATGATCCAGCTGAGACAACTCTATTGTTGTTGA-----CCTCCTG 871
Db 343 GATGTGTTATCAACGAAGAAGCAGAAAATGTATATGTTGATGAGTACTGCGTGTGT 402
Qy 872 AGAAGGGGCGGTCATCGAGTGCCTGTGACAGCCCTTCTCGAGAGCAAGCTTCGC 931
Db 403 GGCATGCGAGGAAATGCTGGACAGCGTGCCGAGAGCGGTTTCCAGATGTGCGAGCCAC 462
Qy 932 CTCTACCTCGGGGAGCTCATCCTGGGCTCGAGTACTTTCACATGCGCAGAAATGCTCCAC 991
Db 463 GGGTACTTCTGTACGTGATTGACGGCTCGAGTACCTGCATGCCAGGCGATTGTGCAC 522
Qy 992 AGGACATCAAGCCATCAACTGCTCTGCGGGGATGATGGGACGTGAAGATCGCCGAC 1051
Db 523 AAGGACATCAAGCGGGGAACTGCTGTCTACCAACCGGTGGCACCTCAAAATCTCCGAC 582
Qy 1052 TTTGGCGTCAGCAACCACTTTGAGGGGAAACAGCTCAGCTGTCCAGCAGCGC-----G 1105
Db 583 CTGGCGGTGGCGGAGCACTGCACCCGTTGCGGGGAGACGACACTGCGCGACGAGCGAG 642
Qy 1106 GGAACCCAGCATTATCGGCCCGAGGCCATTTCTGATTCGGCGCAGAGCTTCAGTGGG 1165
Db 643 GGCTCCCGGCTTTCCAGCCGCCCGAG---ATTCCACCGCCTGGACACCTTTCTCCGGC 699
Qy 1166 AAGCCCTTGGATGATGCGGCACCTGGCGTCACTGTTGTCTATGTTGTTGTTGTTGTTG 1225
Db 700 TTCAAGGTGGACATCTGTCGGCTGGGTCACCCCTCTACAACATCAACACGCGTCTGTAC 759
Qy 1226 CCATTATCAGCATTTTCATCTGCGCCCTCCACAGGAGATCAAGATGAGCCCGTGTG 1285
Db 760 CCCTTCGAAGGGGACACATCTACAAGTTGTTTGAAGAACATCGGGAAGGGAGGTACGCC 819
Qy 1286 TTTCTGAGGAGCCAGAAATCAGCGAGGAGCTCAAGGACCTGATCTCTGAAGATGTTAGAC 1345
Db 820 ATCCCGGGCGACTGTG-----GCCCGCGCTCTCTGACCTGCTGAAGGATCTTTGAG 873
Qy 1346 AAGAATCCGAGACGAGAAATTTGGGTCGCCAGACATCAAGTTGACCTTGGGTGACCAAG 1405
Db 874 TACGAACCGGCCAAGAGGTTCTCCATCCGGCAGATCCGGCAGACACAGCTGTTCCGGAAG 933
Qy 1406 AA 1407
Db 934 AA 935
RESULT 8
US-09-016-434-1146
; Sequence 1146, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; FILING DATE: HEREWITH
; APPLICATION NUMBER: US/09/016,434
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1146:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1302 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: G1480860
US-09-016-434-1146
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Query Match 4.1%; Score 90.4; DB 4; Length 1302;
Best Local Similarity 50.6%; Pred. No. 4.9e-12;
Matches 335; Conservative 0; Mismatches 306; Indels 21; Gaps 4;

QY 758 GTGTACCAAGGAGTCCATCTCTGAAGAAGCTGGACCACTGTAATCTGTCTAACTGATC 817
DB |||||
QY 283 GTGAAGAAGAAATCAACTACTAGGAGGTACGGCACAATAATGTCTCAGCTGGTG 342
DB |||||
QY 818 GAGGTCTCGATGAGCCAGCTGAGGACCACTCTATTTGGTGTGGA-----CCTCTG 871
DB |||||
QY 343 GATGTGTATACAAGAGAGAGAGAAATGTATATGTGATGAGTACTGCGTGTGT 402
DB |||||
QY 872 AGAAGAGGCGCGTCAATGAAGTGCCTGTGACAGCCCTTCTCGGAGAGCAAGCTGCG 931
DB |||||
QY 403 GGCATGCGAAGAAATGCTGACAGCGTGCCTGGAGAGCGTTTCCCACTGTGCGAGCCCA 462
DB |||||
QY 932 CTCCTACCTGCGGAGAGTCTCTCTGCGCTCGAGTACTTCTCACTGCGCAGAAATCTCCAC 991
DB |||||
QY 463 GGTACTTCTGTGCTGATGACGCGCTGGAGTACTCTGATAGCCAGGCAATTTGTCAC 522
DB |||||
QY 992 AGGACATCAAGCCATCAACCTGCTCTCTGGGGATGATGGGCACTGGAAGATCGCCGAC 1051
DB |||||
QY 523 AAGGACATCAAGCGGGGAACCTGCTCTCACACCGGTGGCACCTCAAAATCTCCGAC 582
DB |||||
QY 1052 TTTGGCGTCAGCAACAGTTTGAGGGGAACGAGCTGCTCAGCAGCGC-----G 1105
DB |||||
QY 583 CTGGCGGTGGCGAGGCACTGCACCGGTTCGGCGGAGCACACCTGCGGACCGCCAG 642
DB |||||
QY 1106 GGAACCCAGCACTTCTGCGCCCGGAGGCACTTCTGATTCGGGCGCAGAGCTTCACTGGG 1165
DB |||||
QY 643 GGCTCCCGGCTTTCAGCGCGCCGAG---ATTGCCAAGCGGCTGACACCTTCTCCGCG 699
DB |||||
QY 1166 AAGGCTTTGGATGTATGGGCACTGGCGTCAAGTTGTACTGTCTTCTATGGGAAGTGC 1225
DB |||||
QY 700 TTCAAGGTGGACATCTGGTGGCTGGGGTCACTCTACAACTACCAAGCGGTCTGTAC 759
DB |||||
QY 1226 CAATTCTGAGGATTTCTATCTGCGCTTCCACAGAGATCAAGATGAGCGCGGTGGTG 1285
DB |||||
QY 760 CCTTCGAAGGGGCAACATCTACAAGTTGTTTGAAGATCGGGAAGGGAGCTACGCC 819
DB |||||
QY 1286 TTTCTGAGGAGCCAGAAATCGAGGAGCTCAAGGAGCTGATCTGAGATGTAGAC 1345
DB |||||
QY 820 ATCCCGGCGGACTGTG-----GCCCGCGCTCTCTGACCTCTGAAAGGAGTCTTGAG 873
DB |||||
QY 1346 AAGAAATCCGAGACAGAAATTTGGGTGCGAGACATCAAGTTGACCTTTGGGTGACCAAG 1405
DB |||||
QY 874 TACGAACCGGCAAGAGGTTTCTCCATCCGGCAGATCCGGCAGACAGCTGTTCCGGAAG 933
DB |||||
QY 1406 AA 1407
DB ||
QY 934 AA 935
DB ||

RESULT 9

US-08-749-902-2
Sequence 2, Application US/08749902
Patent No. 5985635
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Goli, Surya K.
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: NOVEL HUMAN SERINE/THREONINE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESS: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: US
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/749,902
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0150 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: Consensus
US-08-749-902-2

Query Match 4.0%; Score 87; DB 2; Length 1466;
Best Local Similarity 50.0%; Pred. No. 3.2e-11;
Matches 331; Conservative 0; Mismatches 310; Indels 21; Gaps 4;

QY 758 GTGTACCAAGGAGTTCATCTCTGAAGAAGCTGGACCACTGTAATGTGGTCTAACTGATC 817
DB |||||
QY 382 GTGAAGAAGAAATCAACTACTAGGAGGTTCACGCAAAAAATGTCTCAGCTGGTG 441
DB |||||
QY 818 GAGGTCTCGATGAGCCAGCTGAGCACAACCTCTATTTGGTGTGGA-----CCTCTG 871
DB |||||
QY 442 GATGTGTATACAAGAGAGAGAGCAAAATGTATATGGTATGAGTACTGCGTGTGT 501
DB |||||
QY 872 AGAAGAGGCGCGTCTCATGGAAGTGCCTGTGACAAGCCCTTCTCGGAGGAGCAAGCTCG 931
DB |||||
QY 502 GGCATGCGAAGAAATGCTGGAAGCTGCGGAGAGCGTTTCCAGTGTGCGGACCGCCAG 561
DB |||||
QY 932 CTCTACTCTCGGAGAGTCACTCTCTGGGCTTCGAGTACTTGCATCTGCCAGAGATCTGTCAC 991
DB |||||
QY 562 GGGTACTTCTGTGAGTCTGATGACGCGCTGCGGTACTGTCATNGCCAGGAGTATGTCAC 621
DB |||||
QY 992 AGGACATCAAGCCATCCAACTGCTCTCTGGGGGATGATGGCAGTGAAGATCCCGAC 1051
DB |||||
QY 622 AAGGCAATCAAGCGGGGAACCTGCTGCTCACACCGGTGGCACCCCTCAAAATCTCCGAC 681
DB |||||
QY 1052 TTTGGCGTCAGCAACCAAGTTTGAGGGGAACGAGCTGCTGAGCAGCAGCGC-----G 1105
DB |||||
QY 682 CTGGCGGTGGCGAGGCACTGCACCGTTGCGGAGAGCGACCACTGCGGACCGCCAG 741
DB |||||
QY 1106 GGAACCCAGCAATTCATGGCCCCCGAGGCAATTTCTGATTCGCGCAGAGCTTCAAGTGG 1165
DB |||||
QY 742 GGTCTCCCGGCTTTCAGCGCGCCGA---NATTGCAACGCGCTCGACACCTTCTCCGCG 798
DB |||||
QY 1166 AAGGCTTTGGATGTATGGGCACTGCGCTGAGTGTGATCTGCTTGTCTATGGGAAGTGC 1225
DB |||||
QY 799 TTCAAGGTGGACATCTGTGCTGGGTTCACCTCTCAACATCACCACGCGGTCTGTAC 858
DB |||||
QY 1226 CCATTCTAGCAGATTTTCATCTCTGCGCTTCCACAGAGAGATCAAGAAATGAGCCCTGTG 1285
DB |||||
QY 859 CCTTCGAAGGGGACAACTCTACAAGTTGTTGAGAACTCGGGAAGGGAGCTACGCC 918
DB |||||
QY 1286 TTTCTGAGGAGCCAGAAATCAGCGAGAGTCTCAAGGACCTGATCTCTGAAATGTAGAC 1345
DB |||||
QY 919 ATCCCGGCGACTGTG-----GCCCGCGCTCTCTGACCTGCTGAAAGGAGTGTGAG 972
DB |||||
QY 1346 AAGATCCGAGAGAGAGATTTGGGTGCGGAGATCAAGTTCACCTTGGGTGAGCCAG 1405
DB |||||
QY 973 TACGAACCGGCAAGAGGTTCTCCATCCGGGAGATCCCGGAGCAGCAGCTGTGTTCCGGAAG 1032
DB |||||

QY 1406 AA 1407
Db 1033 AA 1034

RESULT 10

US-08-685-852-1
; Sequence 1, Application US/08685852
; Patent No. 6660837
; GENERAL INFORMATION:
; APPLICANT: KAIBUCHI, KOZO
; APPLICANT: ONO, YOSHITAKA
; APPLICANT: IWAMATSU, AKIHIRO
; TITLE OF INVENTION: MODIFIED PROTEIN DERIVED FROM PROTEIN KINASE N
; FILE REFERENCE: 016887/0844
; CURRENT APPLICATION NUMBER: US/08/685,852
; CURRENT FILING DATE: 1996-07-24
; PRIOR APPLICATION NUMBER: JP 7-262552
; PRIOR FILING DATE: 1995-09-14
; PRIOR APPLICATION NUMBER: JP 7-344606
; PRIOR FILING DATE: 1995-12-05
; PRIOR APPLICATION NUMBER: JP 8-080549
; PRIOR FILING DATE: 1996-03-08
; PRIOR APPLICATION NUMBER: JP 8-114226
; PRIOR FILING DATE: 1996-04-11
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2968
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (37)..(2862)
US-08-685-852-1

Query Match 3.8%; Score 83.8; DB 4; Length 2968;
Best Local Similarity 54.8%; Pred. No. 2.3e-10;
Matches 166; Conservative 0; Mismatches 137; Indels 0; Gaps 0;
QY 841 GGACAACTCTATTGGTGTGTTGACCTCTGAGAAAGGGGCCCTCATGGAAGTGCCTG 900
Db 2100 GGAGCAGCTGTGCTCGTGTGATGAGTACTCGCGCGTGGGACCTGATGTCACATCCA 2159
QY 901 TGACAAGCCCTTTCGGAGAGCAGCTCGCCTTACCTGGGAGACGTCATCTGGGCGCT 960
Db 2160 CAGCAGCTGTCTCTGAGCCCGTGCCATCTTTTATTCGCCCTGCGTGTGCTGGGCGCT 2219
QY 961 CGAGTACTTGCACTGCCAGAGATCGTCCACAGGAGCATCAAGCCATCCCAACCTGCTCCT 1020
Db 2220 ACAGTTCTTTCAGAAACAGATCGTCTACAGGAGCTGAGTTGGACAAATTTGCTCCT 2279
QY 1021 GGGGGATGATGGGACGCTGAGATCGCCGACTTTGGCGTCAGCAACAGATTTGAGGGAA 1080
Db 2280 GGACACCGAGGGCTACGTCAGATCGCAGACTTTGGGCTCTGCAAGGAGGGGATGGGCTA 2339
QY 1081 CGAGCCTCAGCTGTCAGCAGCGGGAACCCAGACATTCATGGCCCCCGAGGCCATTC 1140
Db 2340 TGGGACCGGACAGCAGCATCTCTGGGACCCCGAGTTCTCTGGCCCTTGAGGTGCTGAC 2399
QY 1141 TGA 1143
Db 2400 GGA 2402

RESULT 11

US-09-256-465-1
; Sequence 1, Application US/09256465
; Patent No. 6043090
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowser

; TITLE OF INVENTION: ANTISENSE MODULATION OF AKT-2 EXPRESSION
; FILE REFERENCE: RFS-0035
; CURRENT APPLICATION NUMBER: US/09/256,465
; CURRENT FILING DATE: 1999-02-23
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 1
; LENGTH: 1599
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (88)..(1533)
US-09-256-465-1

Query Match 3.8%; Score 83.4; DB 3; Length 1599;
Best Local Similarity 51.3%; Pred. No. 2.3e-10;
Matches 254; Conservative 0; Mismatches 226; Indels 15; Gaps 2;
QY 878 GGGCCCCCATGGAAGTGCCTCTGTGACAAGCCCTTCTCGGAGGAGCAAGCTCGCCTCTAC 937
Db 793 GAGCTGTTCTTCCACCTGTCCCGGAGCGTGTCTTACAGAGGAGCGGCCCGGTTTAT 852
QY 938 CTGCGGACGTCATCTCTGGGCTCGAGTACTTGCATGCGCAGAGATCGTCCACAGGAC 997
Db 853 GGTGCAGAGATTGTCTCGGCTCTTGAATCTTGCATCTCGCGGACGCTGTATACCGGAC 912
QY 998 ATCAAGCCATCCCAACCTGCTCTGGGGATGATGGGACGTCGAGATCGCGACTTTGGC 1057
Db 913 ATCAAGCTGGAAACCTCATGCTGGACAAGATGGCCACATCAAGATCACTGACTTTGGC 972
QY 1058 GTCAGCAACCAAGTTTGAGGGGAAACGAGCTCAGCTGTCTCCAGCACGGCGGGAACCCAGCA 1117
Db 973 CTCTGCAAGAGGGCATCAGTGACGGGGCCACCATGAAACCTTCTGTGGACCCCGAG 1032
QY 1118 TTCAATGCCCCCGAGGCCATTTCTGATTCGCGCAGAGCTTTCAGTGGGAAGGCCCTTGAT 1177
Db 1033 TACCTGGGCTGAGGTGCTGGAGGACATGACTA-----TGGCCGGCGCTGGAC 1083
QY 1178 GTATGGCCACTGCGCTCACGTTGTACTGTCTATGGAAGTCCCATTCATCGAC 1237
Db 1084 TGTGGGGGCTGGTGTGTCATGTACGATGATGTGCGCGCCCTGCTCTTACAAC 1143
QY 1238 GATTTCATCTGCGCCTCCACAGGAAGATCAAGAATGAGCCGCTGTGTCTTCTGAGGAG 1297
Db 1144 CAGACCAACGAGCGCCTCTTCGAGCTCATCTCATGGAAGAGATCCGCTTCCC-----G 1197
QY 1298 CAGAAATACGAGGAGCTCAAGGACCTGATCTCTGAAGATGTTAGACAGAAATCCGAG 1357
Db 1198 CGCAGCTCAGCCCCCGAGGCAAGTCCCTGCTTGTGGGCTGCTTAAAGAGGACCCCAAG 1257
QY 1358 ACGAGAATTCGGGTG 1372
Db 1258 CAGAGGCTTGTGGG 1272

RESULT 12

US-09-167-322-3
; Sequence 3, Application US/09167322
; Patent No. 636151
; GENERAL INFORMATION:
; APPLICANT: Allegheny University of the Health
; Sciences, Halpern, Michael S.
; England, James M.
; TITLE OF INVENTION: CANCER VACCINE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seidel, Gonda, Lavorgna & Monaco, P.C.
; STREET: Suite 1800, Two Penn Center Plaza
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19102
; COMPUTER READABLE FORM:


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;
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/167,322
; FILING DATE: 07-Oct-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/00582
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Monaco, Daniel A.
; REGISTRATION NUMBER: 30,480
; REFERENCE/DOCKET NUMBER: 7933-33 PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-8383
; TELEFAX: (215) 568-5549
;
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1599 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-167-322-3

Query Match 3.8%; Score 83.4; DB 4; Length 1599;
Best Local Similarity 51.3%; Pred. No. 2.3e-10;
Matches 254; Conservative 0; Mismatches 226; Indels 15; Gaps 2;

QY 878 GGGCCGTCATGGAAGTGCCTGTGCAAGCCCTTCGAGAGCAAGCTCGCCTCTAC 937
Db 793 GAGCTGTTCTTCCACCTGTCCCGGAGCGTGTCTTCACAGAGGAGCGGCGGTTTAT 852

QY 938 CTGCGGGAGCTCATCTCGGCGCTCGAGTACTTGCACTGCAGAAATCGTCACAGGGAC 997
Db 853 GGTGACAGATTGTCTCGGCTCTTGAGTACTTGCACTCGCGGAGCGTGTATACCGAC 912

QY 998 ATCAAGCCATCAACCTGCTCTCGGGGATGATGGGACGTGAAGATCGCGACTTTGGC 1057
Db 913 ATCAAGCTGGAACCTCATCTGCGGAGTGTGCAAGATGGCCACATCAAGATCACTGCTTGGC 972

QY 1058 GTCAAGAACCTTTGAGGGAAACGACGCTAGCTGTCTCAGACGCGCGGAAACCCAGCA 1117
Db 973 CTCTGCAAGAGGACATCAGTACGCGGCGCACCATGAAACCTTCTGTGGACCCCGGAG 1032

QY 1118 TTCAATGGCCCGGAGGCAATTTCTGATTCGCGCCAGAGCTTCAGTGGGAAGCCCTTGGAT 1177
Db 1033 TACCTGGCGCTGAGGTGCTGGAGGACATGACTA-----TGGCGGCGCGTGGAC 1083

QY 1178 GTATGGCCACCTGGGCTCACTGTTGACTGTTGTCTATGGGAAGTGCCTTCATCGAC 1237
Db 1084 TGGTGGGCGCTGGTGTGTCATGTACGAGATCATGTGCGGCGCGCTGCGCTTCTACAC 1143

QY 1238 GATTTTCATCTGCGCTTCCACAGGAAGATCAGAAATGAGCCCGTGTGTTTCTTAGAGG 1297
Db 1144 CAGGACACGAGCGCTCTTCGAGCTCATCTCCTCATGGAAGAGATCGCTTCCG-----G 1197

QY 1298 CCAGAAATCAGCGAGGAGCTCAAGGACCTGATCCCTGAAGTGTAGCAAGATCCCGAG 1357
Db 1198 CGACGCTCAGCCCCGAGGCGAAGTCCCTGCTGTTGGGTGCTGTTAAGAGGACCCCAAG 1257

QY 1358 ACAGAAATGGGGTG 1372
Db 1258 CAGAGGCTTGGTGGG 1272

RESULT 13
US-09-023-655-1004
; Sequence 1004, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
;
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,655
; FILING DATE: HERewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1004:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1599 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g178325
; US-09-023-655-1004

Query Match 3.8%; Score 83.4; DB 4; Length 1599;
Best Local Similarity 51.3%; Pred. No. 2.3e-10;
Matches 254; Conservative 0; Mismatches 226; Indels 15; Gaps 2;

QY 878 GGGCCGTCATGGAAGTGCCTGTGCAAGCCCTTCGAGAGCAAGCTCGCCTCTAC 937
Db 793 GAGCTGTTCTTCCACCTGTCCCGGAGCGTGTCTTCACAGAGGAGCGGCGGTTTAT 852

QY 938 CTGCGGGAGCTCATCTCGGCGCTCGAGTACTTGCACTGCAGAAATCGTCACAGGGAC 997
Db 853 GGTGACAGATTGTCTCGGCTCTTGAGTACTTGCACTCGCGGAGCGTGTATACCGAC 912

QY 998 ATCAAGCCATCAACCTGCTCTCGGGGATGATGGGACGTGAAGATCGCGACTTTGGC 1057
Db 913 ATCAAGCTGGAACCTCATCTGCGGAGTGTGCAAGATGGCCACATCAAGATCACTGCTTGGC 972

QY 1058 GTCAAGAACCTTTGAGGGAAACGACGCTAGCTGTCTCAGACGCGCGGAAACCCAGCA 1117
Db 973 CTCTGCAAGAGGACATCAGTACGCGGCGCACCATGAAACCTTCTGTGGACCCCGGAG 1032

QY 1118 TTCAATGGCCCGGAGGCAATTTCTGATTCGCGCCAGAGCTTCAGTGGGAAGCCCTTGGAT 1177
Db 1033 TACCTGGCGCTGAGGTGCTGGAGGACATGACTA-----TGGCGGCGCGTGGAC 1083

QY 1178 GTATGGCCACCTGGGCTCACTGTTGACTGTTGTCTATGGGAAGTGCCTTCATCGAC 1237
Db 1084 TGGTGGGCGCTGGTGTGTCATGTACGAGATCATGTGCGGCGCGCTGCGCTTCTACAC 1143

QY 1238 GATTTTCATCTGCGCTTCCACAGGAAGATCAGAAATGAGCCCGTGTGTTTCTTAGAGG 1297
Db 1144 CAGGACACGAGCGCTCTTCGAGCTCATCTCCTCATGGAAGAGATCGCTTCCG-----G 1197

QY 1298 CCAGAAATCAGCGAGGAGCTCAAGGACCTGATCCCTGAAGTGTAGCAAGATCCCGAG 1357
Db 1198 CGACGCTCAGCCCCGAGGCGAAGTCCCTGCTGTTGGGTGCTGTTAAGAGGACCCCAAG 1257

QY 1358 ACAGAAATGGGGTG 1372
Db 1258 CAGAGGCTTGGTGGG 1272

RESULT 13
US-09-023-655-1004
; Sequence 1004, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
;
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,655
; FILING DATE: HERewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1004:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1599 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g178325
; US-09-023-655-1004
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Db 1144 CAGGACACAGAGCCCTCTTCGACTCATCTCTGAAGAGATCCGCTTCCC-----G 1197
Qy 1298 CCAGAAATCAGCAGGAGCTCAAGGACCTGATCTCTGAAGATGTTAGACAAGATCCCGAG 1357
Db 1198 CGCAGCTCAGCCCGAGGCCAAGTCCCTGCTTCTGCTGGCTGCTTAAGAAGGACCCCAAG 1257
Qy 1358 ACAGAAATGGGGTG 1372
Db 1258 CAGAGGCTTGTTGGG 1272

RESULT 14

US-09-799-875-15
; Sequence 15, Application US/09799875
; Patent No. 6638721
; GENERAL INFORMATION:
; APPLICANT: Meyers, Rachel
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: Williamson, Mark
; TITLE OF INVENTION: Therefor
; FILE REFERENCE: 35800/209996
; CURRENT APPLICATION NUMBER: US/09/799,875
; PRIOR FILING DATE: 2001-03-06
; PRIOR APPLICATION NUMBER: 60/182,059
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 09/659,287
; PRIOR FILING DATE: 2000-09-12
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 1257
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-799-875-15

Query Match 3.8%; Score 82.8; DB 4; Length 1257;
Best Local Similarity 53.1%; Pred. No. 3e-10;
Matches 224; Conservative 0; Mismatches 192; Indels 6; Gaps 2;

Qy 758 GTGTACAGGAGATGTCCTCTGAAGAAGCTGGACCACTGTAATGTTGGTCAAACTGATC 817
Db 211 GTCTTCGGGAGCTGGAGATCCTGCAGGAGATCGAGCAGCTTCTCTCTGGTGAACCTCTGG 270
Qy 818 GAGTCTCTGATGATCCAGCTGAGGACAACTCTATTGTTGTTGACCTCTCTGAGAAG 877
Db 271 TACTCTCTCAGGAGAC---GAGGAGGACATGTTATGTCGTGGACCTGCTACTGGGCGGG 327
Qy 878 GGGCCCCGTCATGGAAGTGCCCTGTGACAAGCCCTTCTCGGAGGAGCAAGCTCGCCTCTAC 937
Db 328 GACCTGGCTTACCACCTGCAGCAAGAGCTGCAGTCTCTCCGAGGACACGGTGAAGCTGTAC 387
Qy 938 CTGCGGAGAGTATCTCTGGGCTCGAGTAATTGCACTGCCAGAAGATGTTCCACAGGGAC 997
Db 388 ATCTCGGAGATGGCACTGGCTCTGGAATACTGCGCGGCCAGCACATCATCCACAGAGAT 447
Qy 998 ATCAAGCCATCCAACTGCTCTCGGGGATGATGGGACGTGAGATGCGCGGACTTTGGC 1057
Db 448 GTCAAGCTTGACAACTATCTCTGGATGAGAGGACATGCACACCTGACCGGACTTCAAC 507
Qy 1058 GTCAAGCAACAGTTTGAAGGGAAGCAGCTCAGCTGTCCAGCAGCGGGGAACCCACGCA 1117
Db 508 ATTGCCACCATCATCAAGG---ACGGGAGCGGCGAGCGCATTTAGCAGGACCAACGCG 564
Qy 1118 TTATGCCCCCGAGGCCATTTCTGATTCGGCCAGAGCTTCAGTGGGAAGGCTTGGAT 1177
Db 565 TACATGGCTCCGAGATCTTCCACTCTTTGTTCAACGGCGGACCGGCTACTCTCTCGAG 624
Qy 1178 GT 1179
Db 625 GT 626

RESULT 15

US-09-799-875-13
; Sequence 13, Application US/09799875
; Patent No. 6638721
; GENERAL INFORMATION:
; APPLICANT: Meyers, Rachel
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: Williamson, Mark
; TITLE OF INVENTION: No. 6638721el Human Protein Kinases and Uses
; FILE REFERENCE: 35800/209996
; CURRENT APPLICATION NUMBER: US/09/799,875
; PRIOR FILING DATE: 2001-03-06
; PRIOR APPLICATION NUMBER: 60/182,059
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 09/659,287
; PRIOR FILING DATE: 2000-09-12
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 1826
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (17) ... (1273)
US-09-799-875-13

Query Match 3.8%; Score 82.8; DB 4; Length 1826;
Best Local Similarity 53.1%; Pred. No. 3.4e-10;
Matches 224; Conservative 0; Mismatches 192; Indels 6; Gaps 2;

Qy 758 GTGTACAGGAGATGTCCTCTGAAGAAGCTGGACCACTGTAATGTTGGTCAAACTGATC 817
Db 227 GTCTTCGGGAGCTGGAGATCCTGCAGGAGATCGAGCAGCTTCTCTCTGGTGAACCTCTGG 286
Qy 818 GAGTCTCTGATGATCCAGCTGAGGACAACTCTATTGTTGTTGACCTCTCTGAGAAG 877
Db 287 TACTCTCTCAGGAC---GAGGAGGACATGTTATGTCGTGGACCTGCTACTGGGCGGG 343
Qy 878 GGGCCCCGTCATGGAAGTGCCCTGTGACAAGCCCTTCTCGGAGGAGCAAGCTCGCCTCTAC 937
Db 344 GACCTGGCTTACCACCTGCAGCAGAACTGTCAGTCTCTCCGAGGACACGGTGAAGCTGTAC 403
Qy 938 CTGCGGAGAGTATCTCTGGGCTCGAGTACTTGGACTGCCAGAGATGTTCCACAGGAC 997
Db 404 ATCTCGGAGATGGCACTGGCTCTGGACTACTCTGCGCGGCCAGCACATCATCCACAGAT 463
Qy 998 ATCAAGCCATCCAACTGCTCTCGGGGATGATGGGCACTGTAAGATGCGCGACTTTGGC 1057
Db 464 GTCAAGCTTGACAACTATCTCTGGATGAGAGGACATGCACACTGACCGACTTCAAC 523
Qy 1058 GTCAAGCAACAGTTTGAAGGGAAGCAGCTCAGCTGTCCAGCAGCGGGGAACCCACGCA 1117
Db 524 ATTGCCACCATCATCAAGG---ACGGGAGCGGCGAGCGCATTTAGCAGGACCAACGCG 580
Qy 1118 TTATGCCCCCGAGGCCATTTCTGATTCGGCCAGAGCTTCAGTGGGAAGGCTTGGAT 1177
Db 581 TACATGGCTCCGAGATCTTCCACTCTTTGTTCAACGGCGGACCGGCTACTCTCTCGAG 640
Qy 1178 GT 1179
Db 641 GT 642

Search completed: July 12, 2004, 01:20:51
Job time : 186 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 11, 2004, 17:43:52 ; Search time 1238 Seconds

(without alignments)

7514.987 Million cell updates/sec

Title: US-10-690-617-1

Perfect score: 2190

Sequence: 1 cgcgcggcgctgagctcgg.....ctcttgctattcagacgct 2190

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N Geneseq 29Jan04:*

- 1: geneseqn1980s:*
- 2: geneseqn1990s:*
- 3: geneseqn2000s:*
- 4: geneseqn2001as:*
- 5: geneseqn2001bs:*
- 6: geneseqn2002s:*
- 7: geneseqn2003as:*
- 8: geneseqn2003bs:*
- 9: geneseqn2003cs:*
- 10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	2190	100.0	2190	6	ABL58698
2	2001.6	91.4	3501	5	AAD08635
3	1906.4	87.1	1937	6	AAD30566
4	1636.2	74.7	2711	6	ABK49563
5	1610.2	73.5	2018	6	ABZ11551
6	1601.4	73.1	1611	6	ABX97035
7	1493.8	68.2	1547	6	ABX97034
8	1475.8	67.4	1725	6	ABX97036
9	1461.8	66.7	1542	4	AA306710
10	1366.8	62.4	3411	9	AD553308
11	661	30.2	2545	3	AAZ29223
12	651.2	29.7	4942	9	ADB75227
13	651	29.7	1804	6	ABX92170
14	651	29.7	1804	9	ADB75229
15	645.6	29.5	2056	4	AA157819
16	644	29.4	1767	4	AA44686
17	641.6	29.3	4982	7	ABX34704
18	585.6	26.7	2268	4	AA159606
19	585.6	26.7	2268	4	AA159605
20	572	26.1	731	4	AAH99185
21	561.4	25.6	29629	6	ABL58699
22	529.6	24.2	705	4	AA527190
23	529.6	24.2	705	4	ABK43592

24	529.6	24.2	705	9	ADB93368	Adb93368 Human cdn
25	526	24.0	2411	9	ADC99145	Adc99145 Human KPP
26	518	23.7	1927	4	AAI57820	Aai57820 Human pol
27	395.8	18.1	432	9	ADB85632	Ade85632 Farnesyl
28	389.4	17.8	1854	3	AA78427	Aaa78427 Human sec
29	348.8	15.9	439	4	AAH99412	Aah99412 Human pro
30	283	12.9	331	3	AAC02673	Aac02673 Human sec
31	274.6	12.5	876	6	ABK34394	Abk34394 Human cdn
32	262.6	12.0	491	8	ACH14059	Ach14059 Human adu
33	244.6	11.2	485	8	ACH15568	Ach15568 Human adu
34	202.4	9.2	1174	4	ABL19199	Ab119199 Drosophil
35	201.2	9.2	469	4	AAI15690	Aai15690 Probe #56
36	201.2	9.2	469	4	ABA57768	Aba57768 Human foe
37	201.2	9.2	469	4	AAI37350	Aai37350 Probe #60
38	201.2	9.2	469	4	ABA27140	Aba27140 Probe #56
39	201.2	9.2	469	4	AAK31464	Aak31464 Human bon
40	201.2	9.2	469	4	AAK05833	Aak05833 Human bra
41	201.2	9.2	469	4	ABS31146	Abs31146 Human liv
42	201.2	9.2	469	6	ABS06218	Abs06218 Human gen
43	201.2	9.2	10800	4	AAK83329	Aak83329 Human imm
44	201	9.2	218	4	AAI24914	Aai24914 Probe #14
45	201	9.2	218	4	ABA70385	Aba70385 Human foe

ALIGNMENTS

RESULT 1

ID	ABL58698	standard; cdna; 2190 BP.
XX	ABL58698	
AC	ABL58698	
XX		
DT	27-AUG-2002	(first entry)
XX		
DE	Human kinase encoding cDNA.	
XX		
KW	Human; kinase protein; calcium/calmodulin-dependant protein kinase; eye;	
KW	retinoblastoma; brain; kinase modulator; gene; SNP;	
KW	single nucleotide polymorphism; ss.	
XX		
OS	Homo sapiens.	
XX		
FH	Key	Location/Qualifiers
FT	5'UTR	1..172
FT		/*tag= a
FT	CDS	173..1690
FT		/*tag= b
FT		/*tag= c
FT	variation	/product= "human kinase"
FT		/replace(1296, G)
FT	3'UTR	/*tag= c
FT		/standard name= "single nucleotide polymorphism"
FT		1691..2190
FT		/*tag= d
FT	WO200224920-A2.	
FT	28-MAR-2002.	
FT	19-SEP-2001; 2001WO-US029161.	
FT	19-SEP-2000; 2000US-0233493P.	
FT	13-NOV-2000; 2000US-0247031P.	
FT	06-DEC-2000; 2000US-0072999S.	
FT	(PEKE) PE CORP NY.	
FT	Beasley EM, Wei M, Bonazzi VR, Sanders R, Di Francesco V;	
FT	WPI; 2002-404955/43.	
FT	P-PSDB; ABB83054.	
FT	Novel peptide designated as human kinase useful as target for diagnosing	

PT a disease or predisposition to the disease mediated by the peptide.

XX Claim 4b; Fig 1; 89pp; English.

XX The invention relates to an isolated peptide designated human kinase (HK), that has homology to members of the calcium/calmodulin-dependent protein kinase kinase subfamily. The mechanism of action of the protein of the invention is that of a kinase modulator. The human kinase of the invention is useful for creating a pharmaceutical composition for treating a disease or condition mediated by the human kinase. HK is also useful to provide a target for diagnosing a disease or predisposition to disease mediated by HK, and is also useful in pharmacogenetic analysis. HK is useful for treating a disorder characterised by absence of inappropriate or unwanted expression of HK, also as an immunogen to raise antibodies by administering HK to a mammalian organism e.g. rat, rabbit or mouse. Nucleic acids of the invention are useful as hybridisation probes for mRNA, transcript/cDNA and genomic DNA. Recombinant host cells expressing a native HK are useful for assaying compounds that stimulate or inhibit HK function. Nucleic acids of the invention are also useful for producing transgenic animals. Experimental data indicates that kinase proteins of the present invention are expressed in humans in the eye (retinoblastomas) and brain. The current sequence represents cDNA encoding the human kinase of the invention

SQ Sequence 2190 BP; 457 A; 655 C; 708 G; 370 T; 0 U; 0 Other;

Query Match 100.0%; Score 2190; DB 6; Length 2190;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	CGCCGCGGGCTGAGCTCGGCGATCTGGGCCCCAGCGAGGCGGTGGGGCGGGGCGGCG	60
DB	1	CGCCGCGGGCTGAGCTCGGCGATCTGGGCCCCAGCGAGGCGGTGGGGCGGGGCGGCG	60
QY	61	GGGGGGGGCGGCGAGGAGGAGTGGGGGGCGCGCGCGGCGCCACGACACTGTTCGCC	120
DB	61	GGGGGGGGCGGCGAGGAGGAGTGGGGGGCGCGCGCGGCGCCACGACACTGTTCGCC	120
QY	121	GGGGCGGAGTTCACAGAGCTACGAGAGAACCCCTTGTAGTGAAGCAATGGAGG	180
DB	121	GGGGCGGAGTTCACAGAGCTACGAGAGAACCCCTTGTAGTGAAGCAATGGAGG	180
QY	181	GGGTCCAGTGTCTCTGCGAGGATCTCGGCGAGAGCTGTAGAACGGGTGGCAGCCAT	240
DB	181	GGGTCCAGTGTCTCTGCGAGGATCTCTCGGCGAGAGCTGTAGAACGGGTGGCAGCCAT	240
QY	241	CGATGTGACTCACTTGGAGGAGGAGATGGTGGCCAGAGCTACTAGAAACGGTGTGGA	300
DB	241	CGATGTGACTCACTTGGAGGAGGAGATGGTGGCCAGAGCTACTAGAAACGGTGTGGA	300
QY	301	CCCCCACAAGGCGAGCTGCTGTGATCCCTGGCAGTACTTCAAGACTGCTCCC	360
DB	301	CCCCCACAAGGCGAGCTGCTGTGATCCCTGGCAGTACTTCAAGACTGCTCCC	360
QY	361	AGCCGGGCTAGCTCTCAGCCAGGAAGCTTTCCTCAGGAGCGGCGCAGAGGAGCTA	420
DB	361	AGCCGGGCTAGCTCTCAGCCAGGAAGCTTTCCTCAGGAGCGGCGCAGAGGAGCTA	420
QY	421	TCTGAGGCGCAGGCTGGGCTTTATGCAACGGGGCTGCCAGCCACATCTCCCCCGGGC	480
DB	421	TCTGAGGCGCAGGCTGGGCTTTATGCAACGGGGCTGCCAGCCACATCTCCCCCGGGC	480
QY	481	CTGGCGGAGGCCACCATCGAGTCCACACGTGGCCATCTCAGATGAGAGGCTGCGT	540
DB	481	CTGGCGGAGGCCACCATCGAGTCCACACGTGGCCATCTCAGATGAGAGGCTGCGT	540
QY	541	GCAGTGAACCAAGTACAGAGTGCAGAGTGAGATTGGCAAGGGTGCCTACGGTGTGGTGA	600
DB	541	GCAGTGAACCAAGTACAGAGTGCAGAGTGAGATTGGCAAGGGTGCCTACGGTGTGGTGA	600
QY	601	GCTGGCCCTACAAAGAGTGAAGACAGACACTATGCAATGAAGTCTTCCAAAAGAA	660
DB	601	GCTGGCCCTACAAAGAGTGAAGACAGACACTATGCAATGAAGTCTTCCAAAAGAA	660

QY	661	GTTACTGAGCAGTATGGCTTTCCAGTGGCCCTCCCGGAGAGGGTCCCGAGGCTGCCA	720
DB	661	GTTACTGAGCAGTATGGCTTTCCAGTGGCCCTCCCGGAGAGGGTCCCGAGGCTGCCA	720
QY	721	GGGAGGACACAGCAAGCAGTGTGCGCCCTGGAGCGGTGTACAGAGAGATTGCGCATCCT	780
DB	721	GGGAGGACACAGCAAGCAGTGTGCGCCCTGGAGCGGTGTACAGAGAGATTGCGCATCCT	780
QY	781	GAAGAAGCTGAGCACCACTGTAATGTGGTCAAACTGATCGAGGTCTTGAGATGACCCAGCTGA	840
DB	781	GAAGAAGCTGAGCACCACTGTAATGTGGTCAAACTGATCGAGGTCTTGAGATGACCCAGCTGA	840
QY	841	GGACAACTCTATTGTGTGTGACCTCTGAGAAAGGGGCCCTCATGGAAGTGCCTG	900
DB	841	GGACAACTCTATTGTGTGTGACCTCTGAGAAAGGGGCCCTCATGGAAGTGCCTG	900
QY	901	TGACAAGCCCTCTTCGGAGGAGCAAGCTCGCTCTACTCTGGGACGTCATCTCGGCT	960
DB	901	TGACAAGCCCTCTTCGGAGGAGCAAGCTCGCTCTACTCTGGGACGTCATCTCGGCT	960
QY	961	CGAGTACTTGCACTGCCAGAAGATCGTCCACAGGAGCATCAAGGCATCCACCTGCTCCT	1020
DB	961	CGAGTACTTGCACTGCCAGAAGATCGTCCACAGGAGCATCAAGGCATCCACCTGCTCCT	1020
QY	1021	GGGGGATGATGGGCACGTCGCGACTTTGGGGTTCAGCAACCAAGTTTGAGGGGAA	1080
DB	1021	GGGGGATGATGGGCACGTCGCGACTTTGGGGTTCAGCAACCAAGTTTGAGGGGAA	1080
QY	1081	CGACGCTCAGCTGTCCAGCAGCGCGGGAACCCAGCATTATGGCCCCCGAGGGCCATTTC	1140
DB	1081	CGACGCTCAGCTGTCCAGCAGCGCGGGAACCCAGCATTATGGCCCCCGAGGGCCATTTC	1140
QY	1141	TGATTCGCGCCAGAGCTTTCAGTGGGAAGGCTTGATGTATGGGCACTGCGGTCACGTT	1200
DB	1141	TGATTCGCGCCAGAGCTTTCAGTGGGAAGGCTTGATGTATGGGCACTGCGGTCACGTT	1200
QY	1201	GTACTGTCTGTCTATGGGAAGTCCCATTCATCGACGATTTCTCTGGCCCTCCACAG	1260
DB	1201	GTACTGTCTGTCTATGGGAAGTCCCATTCATCGACGATTTCTCTGGCCCTCCACAG	1260
QY	1261	GAAGATCAAGAAATGAGCCGCTGTTTCTGAGAGCCAGAAATACGCGAGGAGCTCAA	1320
DB	1261	GAAGATCAAGAAATGAGCCGCTGTTTCTGAGAGCCAGAAATACGCGAGGAGCTCAA	1320
QY	1321	GGACTGATCTGAAAGATTTAGACAGAATCCCGAGACGAGATTTGGGGTCCAGACAT	1380
DB	1321	GGACTGATCTGAAAGATTTAGACAGAATCCCGAGACGAGATTTGGGGTCCAGACAT	1380
QY	1381	CAAGTTGCACCTTGGGTGACCAAGAACGGGAGGAGCCCTTCTTCGAGGAGGAGCA	1440
DB	1381	CAAGTTGCACCTTGGGTGACCAAGAACGGGAGGAGCCCTTCTTCGAGGAGGAGCA	1440
QY	1441	CTGAGCGTGTGGAGGTGACAGAGGGGAGGTTAAGAACTCAGTCAGGCTCATCCCCAG	1500
DB	1441	CTGAGCGTGTGGAGGTGACAGAGGGGAGGTTAAGAACTCAGTCAGGCTCATCCCCAG	1500
QY	1501	CTGACCAACGCTGTCTGTGTAAGTCCATGCTGAGGAAGGTTCTTTGGGAACCCGTT	1560
DB	1501	CTGACCAACGCTGTCTGTGTAAGTCCATGCTGAGGAAGGTTCTTTGGGAACCCGTT	1560
QY	1561	TGAGCCCCCAGGACGAGGGAAGAGCGATCCATGTCTCTCCAGGAAACCTTACTGGTGA	1620
DB	1561	TGAGCCCCCAGGACGAGGGAAGAGCGATCCATGTCTCTCCAGGAAACCTTACTGGTGA	1620
QY	1621	AGAGGGGTTTGGTGAAGGGGCAAGAGCCAGAGTCCCCGGGCTCCAGGAAGAGGAGC	1680
DB	1621	AGAGGGGTTTGGTGAAGGGGCAAGAGCCAGAGTCCCCGGGCTCCAGGAAGAGGAGC	1680
QY	1681	TGCATCTCGAGCCCTGCATGACCCAGGGCCACCCGCGACACACTCATCCCGGCGCTC	1740
DB	1681	TGCATCTCGAGCCCTGCATGACCCAGGGCCACCCGCGACACACTCATCCCGGCGCTC	1740

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502 TGCCTACGGTGTGTGAGCTGGCCCTACAAAGAAAGTGAAGACAGACACTATGACATGAA 561
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643 AGTCCTTTTCAAAAAGAGTTACTGAAGCAGTATGGCTTTCCACGTGCGCCCTCCCCCGAG 702
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562 AGTCCTTTTCAAAAAGAGTTACTGAAGCAGTATGGCTTTCCACGTGCGCCCTCCCCCGAG 621
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703 AGGTCCTCAGGCTGCCAGGGAGACACAGCCAGCAGCTGCTGCGCTTGGAGCGGGTGA 762
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622 AGGTCCTCAGGCTGCCAGGGAGACACAGCCAGCAGCTGCTGCGCTTGGAGCGGGTGA 681
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763 CCAGCAGATTGCCATCTCTGAAGAAGCTGACACAGTGAATGTGTCTCAAACTGATCGAGGT 822
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823 CCTGGATGACCCAGCTGAGGACAACTCTATTGCTGTTTGAACCTCTCTGAGAAAGGGGCC 882
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1003 GCCATCCAACTGCTCTCGGGGATGATGGGCACTGTAAGATGCGCGACTTTGGGCTCAG 1062
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1099 GGCCACTGGGCTCAGTTGTAATCTGTTGCTATGGAAGTGCCTCATTCAGCAGATT 1158
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1243 CATCTGCGCCCTCCACAGGAGATCAAGAATGAGCCGCTGCTGCTGAGGAGCCAGA 1302
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1363 AATTGGGCTGACAGATCAAGTTGACCTTGGTGACCAAGAACGGGGAGGAGCCCT 1422
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Db 1579 CGTCCAGGAAGACGAGGCTGCTCCTGAGCCCTGTGATGACACCAGGCGCCACCCCGGACG 1638
Qy 1723 ACATCTATCCCGCGCTTCCAGAGGCCCAACCCCTCATGCAACAGCGCGCCCGCGAGGACG 1782
Db 1639 ACATCTATCCCGCGCTTCCAGAGGCCCAACCCCTCATGCAACAGCGCGCCCGCGAGGACG 1698
Qy 1783 GGGCTGGGACTGACAGCCCACTCCCGCCCTCCCTCCCTCATGCTGATGACTTCCAGCG 1842
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Qy 1843 ACGCAGCTCCAGGGACAGACTGGAAATGATGATCTATTTGGGCTTTGGGGGAGAGGCTCCC 1902
Db 1759 ACGCAGCTCCAGGGACAGACTGGAAATGATGATCTATTTGGGCTTTGGGGGAGAGGCTCCC 1818
Qy 1903 ACGAGGCAATCTCTCTTTTGGCCCTCTTGGCCCTGACCCATTCTGTGGGGAAACCGG 1962
Db 1819 ACGAGGCAATCTCTCTTTTGGACCTCTTGGCCCTGACCCATTCTGTGGGGAAACCGG 1878
Qy 1963 GTGCCCATGGAGCTTCAAGAAATGCACCGGCTGTTGGCATGGCTTGGGGCAGAGGCA 2022
Db 1879 GTGCCCATGGAGCTTCAAGAAATGCACCGGCTGTTGGCATGGCTTGGGGCAGAGGCA 1938
Qy 2023 GAGCAGAGACCAAGATGGCAGGTGAGGCGCAGGCTTACCAACAGGAAGAGACCTCCC 2082
Db 1939 GAGCAGAGACCAAGATGGCAGGTGAGGCGCAGGCTTACCAACAGGAAGAGACCTCCC 1998
Qy 2083 GCTGGGCGCGGCGAGGCTGCTGCTGAGTGGCAGGATATGTTGGAGGGGGGTATCCC 2142
Db 1999 GCTGGGCGCGGCGAGGCTGCTGCTGAGTGGCAGGATATGTTGGAGGGGGGTATCCC 2058
Qy 2143 TGCCCACTTTGGGCTGTTGGCAGGCTTCTGCTATTCAGAGCT 2190
Db 2059 TGCCCACTTTGGGCTGTTGGCAGGCTTCTGCTATTCAGAGCT 2106

RESULT 3
AAD30566
ID AAD30566 standard; cDNA; 1937 BP.
XX AAD30566;
XX
DT 21-MAY-2002 (first entry)
XX
XX Human kinase polypeptide (PKIN-19) cDNA.
XX
DE Human; kinase polypeptide; PKIN-19; gene therapy; Addison's disease;
KW leukaemia; immune disorder; lymphoma; melanoma; developmental disorder;
KW acquired immunodeficiency syndrome; AIDS; allergy; anaemia; hypertension;
KW asthma; Crohn's disease; rheumatoid arthritis; bursitis; atherosclerosis;
KW cirrhosis; hepatitis; psoriasis; Cushing's syndrome; cytostatic; cancer;
KW cholestasis; cardiac; cardiovascular disorder; Niemann-Pick's disease;
KW lipid disorder; fatty liver; Gaucher's disease; myocardial infarction;
KW drug screening; transgenic animal; antiinflammatory; hepatotropic;
KW hypotensive; anti-HIV; enzyme; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 65..1582
FT /*tag= a
FT /product= "Human PKIN-19"
XX
XX WO200208399-A2.
PD 31-JAN-2002.
XX
PF 20-JUL-2001; 2001WO-US023092.
XX
XX 21-JUL-2000; 2000US-0220038P.
PR 28-JUL-2000; 2000US-0222112P.
PR 04-AUG-2000; 2000US-0222831P.
PR 11-AUG-2000; 2000US-0224729P.
XX

PA	(INCY-) INCYTE GENOMICS INC.	Db	382	GCCCAACATCGAGTCCCAACCAACGTCGTCATCTCAGATGCAGAGGACTGCGTGCAGCTGAA	441
PA	(THOR/) THORNTON M.	QY	550	CCAGTACAAAGTCGACAGTGGCAAGGGTGCCTACGGTGTGCTGAGGCTGGCCTA	609
PI	Thornton M, Yue H, Khan FA, Gururajan R, Hafalia AJA, Wallia NK,	Db	442	CCAGTACAAAGTCGACAGTGGCAAGGGTGCCTACGGTGTGCTGAGGCTGGCCTA	501
PI	Patterson C, Ramkumar J, Gandhi AR, Policky JL, Baughn MR;	QY	610	CAACGAAAGTGAAGACAGACATATGCAATGAAAGTCTTTCACAAAAGAAAGTTACTGAA	669
PI	Tribouley CM, Bandman O, Nguyen DB, Lu Y, Burford N, Lal P, Ding L;	Db	502	CAACGAAAGTGAAGACAGACATATGCAATGAAAGTCTTTCACAAAAGAAAGTTACTGAA	561
PI	Yao MG, Elliott VS, Recipon SA, Kearney L, Lu DAM, Greenwald SR;	QY	670	GCAGTATGCTTTCCACGTCGCGCTCCCGGAGAGGGTCCAGGCTGCCAGGAGGACC	729
PI	Tang YT, Xu Y, Walsh RT, Gietzen KJ, Yang J, Hillman JL;	Db	562	GCAGTATGCTTTCCACGTCGCGCTCCCGGAGAGGGTCCAGGCTGCCAGGAGGACC	621
DR	WPI; 2002-206083/26.	QY	730	AGCCAAAGCAGCTGCTGCTCCCTCGAGCGGGTGTACACAGAGATTGCCATCTCTGAAGAAGCT	789
DR	P-PSDB; AAE19161.	Db	622	AGCCAAAGCAGCTGCTGCTCCCTCGAGCGGGTGTACACAGAGATTGCCATCTCTGAAGAAGCT	681
XX	New human kinase polypeptide, useful in diagnosis, prevention and	QY	790	GGACACGCTGAATGTGGTCAAACTGATCGAGGTCTGGATGACCCAGCTGAGGACAACTT	849
XX	treatment of cancer, immune disorder, growth and developmental disorder,	Db	682	GGACACGCTGAATGTGGTCAAACTGATCGAGGTCTGGATGACCCAGCTGAGGACAACTT	741
PT	cardiovascular disorder and lipid disorder.	QY	850	CTATTTGGTGTGGTACCTCTCGAGAAAGGGCCCGTCTATGGAGTGCCTGTGACAGGCC	909
XX	Claim 5; Page 193-194; 196pp; English.	Db	742	CTATTTGGTGTGGTACCTCTCGAGAAAGGGCCCGTCTATGGAGTGCCTGTGACAGGCC	801
CC	The present invention relates to an isolated human kinase polypeptide	QY	910	CTTCTCGAGGAGCAAGCTGCGCTCTTACCTGCGGAGAGCTCATCTCTGGGCTCGAGTACTT	969
CC	(PKIN) or a biologically active/immunogenic fragment of PKIN. PKIN is	Db	802	CTTCTCGAGGAGCAAGCTGCGCTCTTACCTGCGGAGAGCTCATCTCTGGGCTCGAGTACTT	861
CC	useful for diagnosing, treating and preventing cancer (e.g., leukaemia,	QY	970	GCATGCCAGAGATGCTCCACAGGAGCATCAAGCCATCAACCTGCTCTCTGGGGATGA	1029
CC	lymphoma, melanoma), an immune disorder (e.g., acquired immunodeficiency	Db	862	GCATGCCAGAGATGCTCCACAGGAGCATCAAGCCATCAACCTGCTCTCTGGGGATGA	921
CC	syndrome (AIDS), Addison's disease, allergy, anaemia, asthma, Crohn's	QY	1030	TGSGGACGTGAAGTCGCGATCTTGGCGTCAGCACCACTTTGAGGGGAAACGACCTCA	1089
CC	disease, rheumatoid arthritis), a growth and developmental disorder (e.g.	Db	922	TGSGGACGTGAAGTCGCGATCTTGGCGTCAGCACCACTTTGAGGGGAAACGACCTCA	981
CC	buritis, cirrhosis, hepatitis, psoriasis, Cushing's syndrome), a	QY	1090	GCTGTCCAGCACGGGGAAACCCAGCATTCATGCGCCCGAGGCCATTTCTGATTTCCGG	1149
CC	cardiovascular disorder (e.g., atherosclerosis, hypertension, myocardial	Db	982	GCTGTCCAGCACGGGGAAACCCAGCATTCATGCGCCCGAGGCCATTTCTGATTTCCGG	1041
CC	infarction), and a lipid disorder (e.g., fatty liver, cholestasis,	QY	1150	CCAGAGCTTCAGTGGAGAGCCCTTGGATGTATGGGCACTGCGGCTCACTGTGTACTGCTT	1209
CC	Gaucher's disease, Niemann-Pick's disease). PKIN is useful in a number of	Db	1042	CCAGAGCTTCAGTGGAGAGCCCTTGGATGTATGGGCACTGCGGCTCACTGTGTACTGCTT	1101
CC	drug screening techniques and to analyse the proteome of a tissue or cell	QY	1210	TGCTATGGGAGTGCCTTTCATCGAGTTCATCTCTGCGCCCTCCACAGGAGATCAA	1269
CC	type. PKIN is useful for creating knockin humanised animals or transgenic	Db	1102	TGCTATGGGAGTGCCTTTCATCGAGTTCATCTCTGCGCCCTCCACAGGAGATCAA	1161
CC	animals to model human diseases, in somatic or germline gene therapy, to	QY	1270	GAATGAGCCCGTGGTGTTCCTTTCAGGAGCCAGAAATCAGCAGGAGCTCAAGGACCTGAT	1329
CC	generate a transcript image of a tissue or cell type, for detecting	Db	1162	GAATGAGCCCGTGGTGTTCCTTTCAGGAGCCAGAAATCAGCAGGAGCTCAAGGACCTGAT	1221
CC	differences in the chromosomal location due to translocation, inversion,	QY	1330	CTGAGATGTTAGACAGAAATCCCGACAGAGAAATTTGGGTTGCCAGATCAAGTTGCA	1389
CC	etc., among normal, carrier or affected individuals, and as hybridisation	Db	1222	CCTGAAGTGTGAGCAAGAAATCCCGACAGAGAAATTTGGGTTGCCAGATCAAGTTGCA	1281
CC	probes for mapping naturally occurring genomic sequences. PKIN is useful	QY	1390	CCCTTGGGTGACCAAGAACGGGGAGAGCCCTTCTTCTCGGAGGAGGACCTGCGAGCT	1449
CC	in southern or northern analysis, dot blot or other membrane-based	Db	1282	CCCTTGGGTGACCAAGAACGGGGAGAGCCCTTCTTCTCGGAGGAGGACCTGCGAGCT	1341
CC	technologies, in PCR technologies, in dipstick, pin, multiformat enzyme	QY	1450	GGTGGAGGTGACAGAGGGGGAGGTTTAAAGATCAGTCAAGGCTCATCCCCAGCTGACCAAC	1509
CC	linked immunosorbent (ELISA)-like assays and in microarrays utilising	Db	1342	GGTGGAGGTGACAGAGGGGGAGGTTTAAAGATCAGTCAAGGCTCATCCCCAGCTGACCAAC	1401
CC	fluids or tissues from patients to detect altered PKIN expression. The	QY	1510	GGTGTATCTCTGGTGAAGTCCATGCTGAGGAAGCGTTTCTTTTGGGAAACCCGTTTGAAGCCCA	1569
CC	present sequence is human PKIN-19 cDNA	Db	1402	GGTGTATCTCTGGTGAAGTCCATGCTGAGGAAGCGTTTCTTTTGGGAAACCCGTTTGAAGCCCA	1461
XX	Sequence 1937 BP; 425 A; 567 C; 603 G; 342 T; 0 U; 0 Other;	QY	1570	GGCAGGGGAGGAGAGCGATCCATGCTCTGCTCCAGGAAACCTTACTGGTGAAGAGGGTT	1629
XX	Query Match 87.1%; Score 1906.4; DB 6; Length 1937;	Db	1462	AGCACGGGAGGAGAGCGATCCATGCTCTGCTCCAGGAAACCTTACTGGTGAAGAGGGTT	1521
XX	Best Local Similarity 99.7%; Pred. No. 0;				
XX	Matches 1910; Conservative 0; Mismatches 6; Indels 0; Gaps 0;				
QY	130 GTTCCCAACAGGCTACGACAGAAACCCCTTGACTGAAGCAATCGAGGGGGTCCAGC	189			
Db	22 GTTCCCAACAGGCTACGACAGAAACCCCTTGACTGAAGCAATCGAGGGGGTCCAGC	81			
QY	190 TGTCTGTGCTCCAGGATCTCTCGGCGAGAGCTGGTAGAACCGGTGGCAGCCATCGATGTGAC	249			
Db	82 TGTCTGTGCTCCAGGATCTCTCGGCGAGAGCTGGTAGAACCGGTGGCAGCCATCGATGTGAC	141			
QY	250 TCACCTGGAGGAGGAGATGGTGGCCAGAGCTTACTAGAAACGGTGTGGACCCGCCACC	309			
Db	142 TCACCTGGAGGAGGAGATGGTGGCCAGAGCTTACTAGAAACGGTGTGGACCCGCCACC	201			
QY	310 ACGGGCCAGAGTCCCTCTGTGATCCCTGGCAGTACTTCAAGACTGCTCCAGCCCGGCC	369			
Db	202 ACGGGCCAGAGTCCCTCTGTGATCCCTGGCAGTACTTCAAGACTGCTCCAGCCCGGCC	261			
QY	370 TAGCTCTCAGCCAGGAAGCTTTCCCTACAGGAGCGCCAGCAGGAAGCTATCTGAGGC	429			
Db	262 TAGCTCTCAGCCAGGAAGCTTTCCCTACAGGAGCGCCAGCAGGAAGCTATCTGAGGC	321			
QY	430 GCAGGCTGGGCTTATGCCACGGGGCTGCTGAGCCACATCTCTCCCGCGGCTGGCGGAG	489			
Db	322 GCAGGCTGGGCTTATGCCACGGGGCTGCTGAGCCACATCTCTCCCGCGGCTGGCGGAG	381			
QY	490 GCCCACCATCGAGTCCCAACGCTGCGCCATCTCAGATGCAGAGGACTGGTGCAGCTGAA	549			

QY	1630	TGTTGAAGGGGCAAGAGCCACAGAGCTCCCGCGCGTCCAGGAACACAGAGCTGCATCTTG	1689
Db	1522	TGTTGAAGGGGCAAGAGCCACAGAGCTCCCGCGCGTCCAGGAACACAGAGCTGCATCTTG	1581
QY	1690	AGCCCTTGCAATGCAACCAAGGCCACCCGGGAGACACTCATCTCCGCGCTCCAGAGGCC	1749
Db	1582	AGCCCTTGCAATGCAACCAAGGCCACCCGGGAGACACTCATCTCCGCGCTCCAGAGGCC	1641
QY	1750	ACCCCTCATGCAACAGCCGCCCCCGCAGGACAGGGGGCTGGGGACTGCAGAGCCCACTCCG	1809
Db	1642	ACCCCTCATGCAACAGCCGCCCCCGCAGGACAGGGGGCTGGGGACTGCAGAGCCCACTCCG	1701
QY	1810	CCCTCCCCCATCGTGTCTGATGACTCCACGACGACGCTCCAGGACACAGACTGGAATG	1869
Db	1702	CCCTCCCCCATCGTGTCTGATGACTCCACGACGACGCTCCAGGACACAGACTGGAATG	1761
QY	1870	TATGTCAATTTGGGCTCTTTGGGGCAGGGCTCCACAGAGGCCATCCTCTCTTCTTTGGGCC	1929
Db	1762	TATGTCAATTTGGGCTCTTTGGGGCAGGGCTCCACAGAGGCCATCCTCTCTTCTTTGGACC	1821
QY	1930	TCCTTTGSCCTGACCCATTCTGTGGGGAACCGGGTGGCCATGGAGCCTCAGAAATGCCAC	1989
Db	1822	TCCTTTGSCCTGAGCCAATCTGTGGGGAACCGGGTGGCCATGGAGCCTCAGAAATGACAC	1881
QY	1990	CCGGCTGTTGGCATGGCCTTGGGGCAGAGGCAGAGGACGAGACCAAGATGGCAG	2045
Db	1882	CCGGCTGTTGGCATGGCCTTGGGGCAGAGGCAGAGGACGAGACCAAGATGGCAG	1937

RESULT 4

ID	ABK49563
ID	ASK49563 standard; DNA; 2711 BP.
XX	
XX	AC AC
XX	ABK49563;
XX	
DT	15-JUL-2002 (first entry)
XX	
DE	Human cDNA 16002 encoding a novel kinase.
XX	
XX	Human; ss; gene; 16002; kinase; cellular proliferative disorder; cancer;
KW	carcinoma; tumour; adenocarcinoma; haematopoietic neoplastic disorder;
KW	leukemia; lymphoma; brain disorder; cerebral ischaemia; infection;
KW	meningitis; brain abscess; acquire immunodeficiency syndrome; obesity;
KW	AIDS-related myopathy; prion disease; Alzheimer's disease; diabetes;
KW	Parkinson's disease; Huntington's disease; motor neurone disease;
KW	metabolic disorder; anorexia nervosa; pain; inflammation; ischaemia;
KW	irritable bowel syndrome; heart disorder; myocardial infarction;
KW	blood vessel disorder; atherosclerosis; bone metabolism disorder;
KW	osteoporosis; haematopoietic disorder; arthritis.
XX	
OS	Homo sapiens.
XX	
Key	Location/Qualifiers
PH	198..1883
FT	CDS /tag= a
FT	/product= "Kinase 16002"
FT	/note= "This coding sequence (minus the stop codon) is
FT	specifically claimed in claim 1"
XX	
PN	WO200220800-A2.
XX	
PD	14-MAR-2002.
XX	
PF	03-AUG-2001; 2001WO-US024601.
XX	
PR	01-SEP-2000; 2000US-0229299P.
XX	
PA	(MILL-) MILLENNIUM PHARM INC.
XX	
PI	Meyers RA, Silos-Santiago I;
XX	
DR	WPI: 2002-351781/38.

|||||
453 GGCACGGCTGGGGCTTTATGTCACG8GGGCTTGCCAGCCACATCTCCCGCGGCTGGCGG 512
QY
488 AGSCCCACCATCGAGTCCACACACGCGGCCATCTCAGATGCAGAGGACTCGTGCGAGCTG 547
Db
513 AGSCCCACCATCGAGTCCACACACGCGGCCATCTCAGATGCAGAGGACTCGTGCGAGCTG 572
QY
548 AACAGTACAGCTGCAGAGTGAGATTGGCAAGGGTGCCTACCGGTGTGTGAGGCTGGCC 607
Db
573 AACAGTACAGCTGCAGAGTGAGATTGGCAAGGGTGCCTACCGGTGTGTGAGGCTGGCC 632
QY
608 TACAACGAAGTGAAGACACACTATGCAATGAAGTCTTTCCAAAAGAGATTACTG 667
Db
633 TACAACGAAGTGAAGACACACTATGCAATGAAGTCTTTCCAAAAGAGATTACTG 692
QY
668 AAGCAGTATGGCTTTCCACGTGCGCCCTCCCGGAGGGGTCCCGAGGCTGCCAGGGAGGA 727
Db
693 AAGCAGTATGGCTTTCCACGTGCGCCCTCCCGGAGGGGTCCCGAGGCTGCCAGGGAGGA 752
QY
728 CCAGCCAGCAGCTGCTGCGCCCTGGAGCGGGTGTACAGAGAGATTGCTCCTGAAGAAG 787
Db
753 CCAGCCAGCAGCTGCTGCGCCCTGGAGCGGGTGTACAGAGAGATTGCTCCTGAAGAAG 812
QY
788 CTGGACACGTGAATGTGGTCAAACTGATCGAGGTCTTGATGACCCAGCTGAGGACAC 847
Db
813 CTGGACACGTGAATGTGGTCAAACTGATCGAGGTCTTGATGACCCAGCTGAGGACAC 872
QY
848 CTCTATTTGGTGTGTTGACCTCTGAGAAAGGGGCCGTGATGAAGTGCCTGTGACAAG 907
Db
873 CTCTATTTGGTGTGTTGACCTCTGAGAAAGGGGCCGTGATGAAGTGCCTGTGACAG 932
QY
908 CCTTCTCGAGGAGCAAGTGCCTCTTACCTGGGGAAGTCAATCTGGGCTCGAGTAC 967
Db
933 CCTTCTCGAGGAGCAAGTGCCTCTTACCTGGGGAAGTCAATCTGGGCTCGAGTAC 992
QY
968 TTGCACTGCGAGAAGATCGTCCACAGGACATCAAGCCATCCAACTGCTCCTGGGGGAT 1027
Db
993 TTGCACTGCGAGAAGATCGTCCACAGGACATCAAGCCATCCAACTGCTCCTGGGGGAT 1052
QY
1028 GATGGCAGCTGAAGATCGCCGACTTTGGCGTCAGCAACCAAGTTTCAGGGGAAACGAGCT 1087
Db
1053 GATGGCAGCTGAAGATCGCCGACTTTGGCGTCAGCAACCAAGTTTCAGGGGAAACGAGCT 1112
QY
1088 CAGCTGTCAGACGCGGGGAACCCAGCATTCATGGCCCCAGGCCATTTCTGATTC 1147
Db
1113 CAGCTGTCAGACGCGGGGAACCCAGCATTCATGGCCCCAGGCCATTTCTGATTC 1172
QY
1148 GGCAGAGCTTCAGTGGGAAGGCTTTGGATGTATGGGCCACTGGCGTCACTGTTACTGC 1207
Db
1173 GGCAGAGCTTCAGTGGGAAGGCTTTGGATGTATGGGCCACTGGCGTCACTGTTACTGC 1232
QY
1208 TTTGTCTATGGGAAGTGCCCAITTCAGCAGATTTTCATCTGGCCCTCCACAGGAAGATC 1267
Db
1233 TTTGTCTATGGGAAGTGCCCGTTTCATCGACGATTTTCATCTGGCCCTCCACAGGAAGATC 1292
QY
1268 AAGATGACCCGTGTGTGTTCTTAGGAGCGCAAGAAATCAGCAGAGCTCAAGGACCTG 1327
Db
1293 AAGATGACCCGTGTGTGTTCTTAGGAGCGCGCAAGAAATCAGCAGAGCTCAAGGACCTG 1352
QY
1328 ATCTCAAGATGTTAGACAGAGATCCGAGACGAGAAATTTGGGTGCGCAGCATCAAGTTG 1387
Db
1353 ATCTCAAGATGTTAGACAGAGATCCGAGACGAGAAATTTGGGTGCGCAGCATCAAGTTG 1412
QY
1388 CACCTTTGGGTGACCAAGAACGGGAGGAGCCCTTCCTTCGAGAGGAGGACACTCGAGC 1447
Db
1413 CACCTTTGGGTGACCAAGAACGGGAGGAGCCCTTCCTTCGAGAGGAGGACACTCGAGC 1472
QY
1448 GTGGTGGAGGTGACAGAGGGGAGGTTAAGAACTCAGTCAAGGCTCATCCAGCTGGAC 1507
Db
1473 GTGGTGGAGGTGACAGAGGGGAGGTTAAGAACTCAGTCAAGGCTCATCCAGCTGGAC 1532
QY
1508 ACGGTGATCTGTGTAAGTCCATGCTGAGGAGCGTTCTTTGGGAACCGGTTTGAGGCC 1567
|||||

Db 1533 ACGGTGATCTGTGTAAGTCCATGCTGAGGAAGCGTTCTTTGGGAACCGGTTTGAGCCC 1592
QY 1568 CAGGCACGGAGGGAAGAGCGATCCATGTCTGTCTCCAGGAAACCTACTGGTGAAGAAGGG 1627
Db 1593 CAAGCAOAGGAGGGAAGAGCGATCCATGTCTGTCTCCAGGAAACCTACTGGTGAAGAAGGG 1652
QY 1628 TTTGGTGAAGGGGGCAAGAGCCAGAGCTCCCGCGGTCCAGGAAGACGA 1677
Db 1653 TTTGGTGAAGGGGGCAAGAGCCAGAGCTCCCGCGGTCCAGGCTTACCA 1702
RESULT 5
ABZ11551
ID ABZ11551 standard; cDNA; 2018 BP.
XX
AC ABZ11551;
XX
DT 20-JAN-2003 (first entry)
XX
Human polynucleotide SEQ ID NO 433.
XX
Human; genome mapping; gene therapy; food supplement; virus; fungus;
cell-proliferative disorder; neurodegenerative disease; bacterial;
Parkinson's disease; Alzheimer's disease; autoimmune disease;
multiple sclerosis; diabetes; genetic disorder; wound; burn; infection;
arthritis; cytostatic; immunomodulator; nootropic; neuroprotective;
antiparkinsonian; antidiabetic; immunosuppressive; dermatological;
haemostatic; vulnery; fungicide; anticancer; virucide; protozoicide;
antiarthritic; gene; ss.
XX
Homo sapiens.
OS
XX
PN WO200270539-A2.
PD 12-SEP-2002.
XX
PF 05-MAR-2002; 2002WO-US005095.
XX
PR 05-MAR-2001; 2001US-00799451.
XX
PA (HYSE-) HYSEQ INC.
PI Tang YT, Zhou P, Goodrich RW, Asundi V, Zhang J, Zhao QA, Ren F;
PI Xue AJ, Yang Y, Ma Y, Yamazaki V, Chen R, Wang Z, Ghosh M;
PI Wehrman T, Wang J, Wang D, Drmanac RT;
XX
DR WPI: 2002-759812/82.
DR P-PSDB; ABP69334.
XX
PT New polynucleotides comprising sequences assembled from expressed
sequence tags (ESTs), useful for treating cell-proliferative,
neurodegenerative, autoimmune, genetic, myeloid or lymphoid, or platelet
or coagulation disorders.
PT
XX
PS Claim 1; SEQ ID NO 433; 1012pp + Sequence Listing; English.
XX
The invention relates to an isolated polynucleotide (1) comprising a
nucleotide sequence selected from any of 948 sequences (ABZ11119-
CC ABZ12066) or their mature protein coding portion, active domain coding
protein or complementary sequences. The polynucleotides are useful for
identifying expressed genes or for physical mapping of human genome. The
encoded polypeptides (ABP6902-ABP6949) are useful as molecular weight
markers, as a food supplement, for generating antibodies, in medical
imaging, screening and diagnostic assays and for treating cell-
proliferative disorders (cancer), neurodegenerative diseases (Parkinson's
or Alzheimer's disease), autoimmune diseases (multiple sclerosis,
diabetes, lupus) genetic disorders, myeloid or lymphoid disorders,
platelet or coagulation disorders, wound, burns, incision, ulcers, liver
or lung fibrosis, infections (bacterial, viral, fungal, parasitic),
arthritis, etc. Note: The sequence data for this patent did not form part
of the printed specification, but was obtained in electronic format
directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX

SQ	Sequence	2018 BP; 453 A; 600 C; 603 G; 362 T; 0 U; 0 Other;
	Query Match	73.5%; Score 1610.2; DB 6; Length 2018;
	Best Local Similarity	98.3%; Pred. No. 0;
	Matches 1638; Conservative	0; Mismatches 28; Indels 1; Gaps 1;
QY	129	GGTTCCCAACAGGCTACGACAGAGAACCCCTTGTGACTGAGCAATCGAGGGGGTCCAG 188
DB	188	GGTTCCCAACAGGCTACGACAGAGAACCCCTTGTGACTGAGCAATCGAGGGGGTCCAG 247
QY	189	CTGTCTGTCCAGGATCTCCGGCAGAGCTGGTAGAACGGGTGGCAGCCATCGATGTGA 248
DB	248	CTGTCTGTCCAGGATCTCCGGCAGAGCTGGTAGAACGGGTGGCAGCCATCGATGTGA 307
QY	249	CTCACTTGGAGGAGGCGAGATGGTGGCCCGACAGCCCTACTAGAAACGGTGTGAGCCCCAC 308
DB	308	CTCACTTGGAGGAGGCGAGATGGTGGCCCGACAGCCCTACTAGAAACGGTGTGAGCCCCAC 367
QY	309	CACGGGCCAGAGCTGCTCTGTGATCCCTGGCAGTACTTCAAGACTGCTCCAGCCCGGC 368
DB	368	CACGGGCCAGAGCTGCTCTGTGATCCCTGGCAGTACTTCAAGACTGCTCCAGCCCGGC 427
QY	369	CTAGCCTCTCAGCCAGGAGCTTTTCCCTACAGGAGCGGCCAGCAGGAGCTATCTGGAGG 428
DB	428	CTAGCCTCTCAGCCAGGAGCTTTTCCCTACAGGAGCGGCCAGCAGGAGCTATCTGGAGG 487
QY	429	CGZAGGCTGGGCTTATGCGACGGGCTGCGACGACATCTCCCGCGGSCCTGGCGGA 488
DB	488	CGCAGGCTGGGCTTATGCGACGGGCTGCGACGACATCTCCCGCGGSCCTGGCGGA 547
QY	489	GGCCCCACCATCGAGTCCACACAGTGGCCATCTCAGATGCGAGAGACTGCGCTGCAGCTGA 548
DB	548	GGCCCCACCATCGAGTCCACACAGTGGCCATCTCAGATGCGAGAGACTGCGCTGCAGCTGA 607
QY	549	ACCAAGTACAAGGTGCGAGAGTGGCAAGGGTGCCTACGGTGTGTGTGAGGCTGGCCT 608
DB	608	ACCAAGTACAAGGTGCGAGAGTGGCAAGGGTGCCTACGGTGTGTGTGAGGCTGGCCT 667
QY	609	ACAAGAAAGTGAAGACAGACATATGCAATGAAGTCCCTTCCMAAAGAAAGTACTGA 668
DB	668	ACAAGAAAGTGAAGACAGACATATGCAATGAAGTCCCTTCCMAAAGAAAGTACTGA 727
QY	669	AGCAGTATGGCTTTCCAGTGGCCCTCCCGCAGAGGGTCCAGGCTCCCGCAGGAGGAC 728
DB	728	AGCAGTATGGCTTTCCAGTGGCCCTCCCGCAGAGGGTCCAGGCTCCCGCAGGAGGAC 787
QY	729	CAGCCAAGCAGCTGCTGCCCTCGAGCGGGTGTACCAAGAGATTGCCATCTCTGAAGAAGC 788
DB	788	CAGCCAAGCAGCTGCTGCCCTCGAGCGGGTGTACCAAGAGATTGCCATCTCTGAAGAAGC 847
QY	789	TGGACCACTGAATGTGTGTAATCTGATCGAGGTCTTGATGATGCCAGCTGAGNCAACC 848
DB	848	TGGACCACTGAATGTGTGTAATCTGATCGAGGTCTTGATGATGCCAGCTGAGNCAACC 907
QY	849	TCTATTTGGTGTGTGACCTCTGAGAAAGGGCCCGCTCATGGAAGTGCCTGTGACAAGC 908
DB	908	TCTATTTGGTGTGTGACCTCTGAGAAAGGGCCCGCTCATGGAAGTGCCTGTGACAAGC 967
QY	909	CTTCTCGGAGGAGCAAGCTCGCCTCTACTCTGCGGAGCGTCACTCTGGGCTCTGAGTACT 968
DB	968	CTTCTCGGAGGAGCAAGCTCGCCTCTACTCTGCGGAGCGTCACTCTGGGCTCTGAGTACT 1027
QY	969	TGCACTGCCAGAGATCTGCACAGGGACATCAAGCCATCAACTGCTCTCTGGGGGATG 1028
DB	1028	TGCACTGCCAGAGATCTGCACAGGGACATCAAGCCATCAACTGCTCTCTGGGGGATG 1087
QY	1029	ATGGCAGCTGAAGATCGCGCATTTTGGCGTTCAGCAACCAAGTTTGAGGGGACACGCTC 1088
DB	1088	ATGGCAGCTGAAGATCGCGCATTTTGGCGTTCAGCAACCAAGTTTGAGGGGACACGCTC 1147
QY	1089	AGCTGTCCAGACCGCGGGAAACCCAGCATTCATGGCCCCCGAGGCCATTTCTGATTCCG 1148
DB	1148	AGCTGTCCAGACCGCGGGAAACCCAGCATTCATGGCCCCCGAGGCCATTTCTGATTCCG 1207

QY	1149	GCCAGAGCTTCAGTGGGAAGSCCTTGGATGTATGGCCACTGGCGTCACGTTTACTGCT 1208
DB	1208	GCCAGAGCTTCAGTGGGAAGSCCTTGGATGTATGGCCACTGGCGTCACGTTTACTGCT 1267
QY	1209	TTGTCTATGGGAAGTGCCTTTCATCGACGATTTTCATCTTGGCCCTCCACAGGAAGATCA 1268
DB	1268	TTGTCTATGGGAAGTGCCTTTCATCGACGATTTTCATCTTGGCCCTCCATAGGAAGATCA 1327
QY	1269	AGAATGAGCCCGTGGTGTTCCTGAGAGCCGAAATCAGGAGGAGCTCAAGAACCTGA 1328
DB	1328	AGAATGAGCCCGTGGTGTTCCTGAGAGCCGAAATCAGGAGGAGCTCAAGAACCTGA 1387
QY	1329	TCCTGAAGATGTTAGACAAGAAATCCCGAGACGAAATTTGGGTGCCAGACATCAAGTTGC 1388
DB	1388	TCCTGAAGATGTTAGACAAGAAATCCCGAGACGAAATTTGGGTGCCAGACATCAAGTTGC 1447
QY	1389	ACCTTTGGGTGCACCAAGAAACGGGAGGAGCCCTTCTTCCTCGAGGAGGAGCACTGCAGCG 1448
DB	1448	ACCTTTGGGTGCACCAAGAAACGGGAGGAGCCCTTCTTCCTCGAGGAGGAGCACTGCAGCG 1507
QY	1449	TGTTGAGGTGACAGAGGGGAGGTTAAGAACTCAGTCAGGCTCATCCCGAGCTGGACCA 1508
DB	1508	TGTTGAGGTGACAGAGGGGAGGTTAAGAACTCAGTCAGGCTCATCCCGAGCTGGACCA 1567
QY	1509	CGGTGATCTTGTGAAAGTCCATGCTGAGGAAGCGTTCTTTGGGAAACCCGTTTGAGCCCC 1568
DB	1568	CGGTGATCTTGTGAAAGTCCATGCTGAGGAAGCGTTCTTTGGGAAACCCGTTTGAGCCCC 1627
QY	1569	AGGCACGAGGAGGAAAGCGATCCATGTCTGCTCCAGGAAACCTACTGGTGAAGAAAGGT 1628
DB	1628	AAGCACGAGGAGGAAAGCGATCCATGTCTGCTCCAGGAAACCTACTGGTGAAGAAAGGT 1687
QY	1629	TTGTGAAGGGGGCAAGAGCCAGACTCCCGCGCTCCAGGAAGAGGCTGCATCCT 1688
DB	1688	TTGTGAAGGGGGCAAGAGCCAGACTCCCGCGCTCCAGGAAGAGGCTGCATCCT 1747
QY	1689	GAGCCCTTGCATGCAACCCAGGGCCACCCGCGCAGCACACTCATCCGCGCTCCAGAGGCC 1748
DB	1748	GAGCCCTTGCATGCAACCCAGGGCCACCCGCGCAGCACACTCATCCGCGCTCCAGAGGCC 1806
QY	1749	CACCCCTCATGCAACAGCGCCCGCCGAGGAGCGGGGCTGGGAGCTG 1795
DB	1807	CCCAACCTCAATCAACAGCGCCCGCCGCAAGGCCAGGGGGGCTG 1853

RESULT 6
ABX97035

ID ABX97035 standard; cDNA; 1611 BP.

AC ABX97035;

XX 20-MAY-2003 (first entry)

DE Human NOV15b cDNA.

KW NOVX; cytostatic; cardiant; arteriosclerotic; antiasthmatic; cancer;
hypotensive; cardiomyopathy; bronchial asthma; gene therapy; vaccine;
human; gene; ss.

OS Homo sapiens.

PN WO200272757-A2.

XX 19-SEP-2002.

PF 08-MAR-2002; 2002MO-US006908.

PR 08-MAR-2001; 2001US-0274101P.

PR 08-MAR-2001; 2001US-0274194P.

PR 08-MAR-2001; 2001US-0274281P.

PR 08-MAR-2001; 2001US-0274322P.

PR 09-MAR-2001; 2001US-0274849P.

PR 12-MAR-2001; 2001US-0275235P.
PR 13-MAR-2001; 2001US-0275578P.
PR 13-MAR-2001; 2001US-0275579P.
PR 13-MAR-2001; 2001US-0275601P.
PR 14-MAR-2001; 2001US-0276000P.
PR 16-MAR-2001; 2001US-0276776P.
PR 19-MAR-2001; 2001US-0276994P.
PR 20-MAR-2001; 2001US-0277239P.
PR 20-MAR-2001; 2001US-0277321P.
PR 20-MAR-2001; 2001US-0277327P.
PR 21-MAR-2001; 2001US-0277791P.
PR 22-MAR-2001; 2001US-0277831P.
PR 23-MAR-2001; 2001US-0278152P.
PR 26-MAR-2001; 2001US-0278894P.
PR 27-MAR-2001; 2001US-0278999P.
PR 27-MAR-2001; 2001US-0279036P.
PR 28-MAR-2001; 2001US-0279344P.
PR 30-MAR-2001; 2001US-0277338P.
PR 30-MAR-2001; 2001US-0279995P.
PR 30-MAR-2001; 2001US-0280233P.
PR 02-APR-2001; 2001US-0280802P.
PR 02-APR-2001; 2001US-0280822P.
PR 02-APR-2001; 2001US-0280900P.
PR 03-APR-2001; 2001US-0281194P.
PR 13-APR-2001; 2001US-0283675P.
PR 30-APR-2001; 2001US-0287424P.
PR 02-MAY-2001; 2001US-0288066P.
PR 03-MAY-2001; 2001US-0288342P.
PR 03-MAY-2001; 2001US-0288528P.
PR 15-MAY-2001; 2001US-0291190P.
PR 16-MAY-2001; 2001US-0291099P.
PR 16-MAY-2001; 2001US-0291240P.
PR 30-MAY-2001; 2001US-0294485P.
PR 31-MAY-2001; 2001US-0294889P.
PR 31-MAY-2001; 2001US-0294899P.
PR 18-JUN-2001; 2001US-0299027P.
PR 19-JUN-2001; 2001US-0299303P.
PR 19-JUN-2001; 2001US-0299310P.
PR 10-JUL-2001; 2001US-0304354P.
PR 31-JUL-2001; 2001US-0309198P.
PR 16-AUG-2001; 2001US-0312903P.
PR 10-SEP-2001; 2001US-0318462P.
PR 12-SEP-2001; 2001US-0318770P.
PR 27-SEP-2001; 2001US-0325430P.
PR 27-SEP-2001; 2001US-0325681P.
PR 18-OCT-2001; 2001US-0330380P.
PR 31-OCT-2001; 2001US-0335301P.
PR 14-NOV-2001; 2001US-0332172P.
PR 14-NOV-2001; 2001US-0332271P.
PR 14-NOV-2001; 2001US-0332272P.
PR 14-NOV-2001; 2001US-0333184P.
PR 14-NOV-2001; 2001US-0333272P.
PR 21-NOV-2001; 2001US-0332094P.
PR 03-DEC-2001; 2001US-0337426P.
PR 03-DEC-2001; 2001US-0338092P.
PR 04-DEC-2001; 2001US-0337185P.
PR 03-JAN-2002; 2002US-0345705P.
PR 07-MAR-2002; 2002US-00092900.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Padigar M, Spytek KA, Shenoy SG, Taupier RJ, Pena CEA, Li L;
PI Zernusen BD, Gusev V, Ji W, Gorman L, Miller CE, Kekuda R;
PI Patturajan M, Gangoli E, Vernet CAM, Guo X, Tcherniev V;
PI Fernandes ER, Casman SJ, Malyankar UM, Gerlach V, Liu Y, Anderson D;
PI Spaderna SK, Catterton E, Burgess C, Leite M, Zhong H, Alsobrook JP;
PI Lepley DM, Rieger DK,
XX
XX WPI; 2002-723332/78.
DR P-PSDB; ABU65068.
XX
XX NOVX polypeptides and polynucleotides, useful for preventing or treating
PT a disorder associated with aberrant NOVX expression or activity e.g.,

PT cancer, hypertension, atherosclerosis, cardiomyopathy or bronchial
PT asthma.
XX
XX Claim 13; Page 139; 1103pp; English.
XX
XX This invention describes novel human NOVX polypeptides which have
CC cytosolic, cardiant, antiarteriosclerotic, antiasthmatic and hypotensive
CC activity. Pharmaceutical compositions comprising the NOVX proteins or
CC nucleic acid molecules or NOVX antibodies are useful for preventing or
CC treating a disorder associated with aberrant NOVX expression or activity
CC e.g. cancer, hypertension, atherosclerosis, cardiomyopathy or bronchial
CC asthma. The products of the invention can be used for gene therapy or in
CC a vaccine. ABX97008-ABX97185 are cDNA fragments amplified and isolated by
CC the PCR primers and probes represented in ABX13460-ABX13462 and ABX97186-
CC ABX97593. ABX97008-ABX97185 encode the NOVX proteins described in
CC ABU65041-ABU65218
XX
SQ Sequence 1611 BP; 366 A; 461 C; 497 G; 287 T; 0 U; 0 Other;
Query Match 73.1%; Score 1601.4; DB 6; Length 1611;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1605; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 122 GCGCCAGGTTCCCAACAGGCTACGCACAGAACCCCTTGACTGAAGCAATGGAGGG 181
Db 1 GCGCCAGGTTCCCAACAGGCTACGCACAGAACCCCTTGACTGAAGCAATGGAGGG 60
QY 182 GGTCCAGCTGTCTGCTGCCAGGATCCTCGGCAGAGCTGTGTAACGGGTGGCAGGCATC 241
Db 61 GGTCCAGCTGTCTGCTGCCAGGATCCTCGGCAGAGCTGTGTAACGGGTGGCAGGCATC 120
QY 242 GATGTGACTCACTTGGAGGAGGCAGATGTTGGCCAGAGCTTACTAGAACGGTGTGGAC 301
Db 121 GATGTGACTCACTTGGAGGAGGCAGATGTTGGCCAGAGCTTACTAGAACGGTGTGGAC 180
QY 302 CCCCCACACAGGCGGCAGAGCTGCTGTGATCCCTGGCAGTACTTCAAGACTGTCCCA 361
Db 181 CCCCCACACAGGCGGCAGAGCTGCTGTGATCCCTGGCAGTACTTCAAGACTGTCCCA 240
QY 362 GCCCGGCTTAGCTCTCAGCCAGGAGCTTCCCTACAGAGCGGCAGCCAGCAAGCTAT 421
Db 241 GCCCGGCTTAGCTCTCAGCCAGGAGCTTCCCTACAGAGCGGCAGCCAGCAAGCTAT 300
QY 422 CTGGAGGCGCAGCTGGGCTTTATGCCAGGGGCTTCCAGCCACATCTCCCCCGGGCC 481
Db 301 CTGGAGGCGCAGCTGGGCTTTATGCCAGGGGCTTCCAGCCACATCTCCCCCGGGCC 360
QY 482 TGGCGGAGGCCACCATCGAGTCCACACGCTGGGCATCTCAGATGCAGAGACTGCGTG 541
Db 361 TGGCGGAGGCCACCATCGAGTCCACACGCTGGGCATCTCAGATGCAGAGACTGCGTG 420
QY 542 CAGCTGAACCCAGTACAAGCTGCAGAGTGAAGTGGCAAGGGTCCCTACGGTGTGGAGG 601
Db 421 CAGCTGAACCCAGTACAAGCTGCAGAGTGAAGTGGCAAGGGTCCCTACGGTGTGGAGG 480
QY 602 CTGGCTTACAACGAAGTGAAGACAGACACTATGCAATGAAGTCTTTTCCAAAAGAG 661
Db 481 CTGGCTTACAACGAAGTGAAGACAGACACTATGCAATGAAGTCTTTTCCAAAAGAG 540
QY 662 TTACTGAAGCAGTATGGCTTTTCCAGTGGCTTCCCGGAGGGTCCAGGCTGCCAG 721
Db 541 TTACTGAAGCAGTATGGCTTTTCCAGTGGCTTCCCGGAGGGTCCAGGCTGCCAG 600
QY 722 GGAGCAGCAGCAACAGCAGCTGTGCGCTCGAGGGGTGTACACAGAGATTGCCATCTG 781
Db 601 GGAGCAGCAGCAACAGCAGCTGTGCGCTCGAGGGGTGTACACAGAGATTGCCATCTG 660
QY 782 AAGAGCTGGACCAAGTGAATGTGTCAACTGATCGAGGCTCTGGATGACCCAGCTGAG 841
Db 661 AAGAGCTGGACCAAGTGAATGTGTCAACTGATCGAGGCTCTGGATGACCCAGCTGAG 720
QY 842 GACAACTCTATTGGTGTGATCCCTCTGAGAAAGGGCGCGTCAATGGAAGTGCCTGT 901
Db 720 GACAACTCTATTGGTGTGATCCCTCTGAGAAAGGGCGCGTCAATGGAAGTGCCTGT 841

Db 721 GACAACTCTATTGTTGTTGACCTCTCTGAGAAAGGGCCCGTCATGGAAGTGCCTCTGT 780
Qy 902 GACAAGCCCTTCTCGAGGAGCAAGCTGCGCTCTTACTGCGGAGCGTCACTCTGGGCTC 961
Db 781 GACAAGTCTTCTCGAGGAGCAAGCTGCGCTCTTACTGCGGAGCGTCACTCTGGGCTC 840
Qy 962 GAGTACTTGCATCTGCGAGAGATCGTCCACAGGACATCAAGCCATCCAACCTGCTCTG 1021
Db 841 GAGTACTTGCATCTGCGAGAGATCGTCCACAGGACATCAAGCCATCCAACCTGCTCTG 900
Qy 1022 GGGGATGATGGGCAAGTGAAGATCGCCGACCTTGGCGTCAGCAACCAAGTTTGAAGGAA 1081
Db 901 GGGGATGATGGGCAAGTGAAGATCGCCGACCTTGGCGTCAGCAACCAAGTTTGAAGGAA 960
Qy 1082 GACCTCAGCTGTTCAGCAACCGGGGAAACCCAGCATTCATGGCCCGGAGGCCATTCT 1141
Db 961 GACGCTCAGCTGTTCAGCAACCGGGGAAACCCAGCATTCATGGCCCGGAGGCCATTCT 1020
Qy 1142 GATTCCGSCCAGAGCTTCAGTGGGAAAGCCCTTGGATGTATGGGCCACTTGGCGTCAAGTTG 1201
Db 1021 GATTCCGSCCAGAGCTTCAGTGGGAAAGCCCTTGGATGTATGGGCCACTTGGCGTCAAGTTG 1080
Qy 1202 TACTGCTTTGTCTATGGAAAGTGCCTATTCAGCAAGATTTTCATCTGGCCCTCCACAGG 1261
Db 1081 TACTGCTTTGTCTATGGAAAGTGCCTATTCAGCAAGATTTTCATCTGGCCCTCCACAGG 1140
Qy 1262 AAGATCAAGATGAGCCGCTGCTTCTGAGGAGCCAGAAATCAGGAGAGGCTCAAG 1321
Db 1141 AAGATCAAGATGAGCCGCTGCTTCTGAGGAGCCAGAAATCAGGAGAGGCTCAAG 1200
Qy 1322 GACCTGATCCTGAGATGTTAGACAAGAAATCCGAGAGGAGTGGGTTGGGTTGCCAGATC 1381
Db 1201 GACCTGATCCTGAGATGTTAGACAAGAAATCCGAGAGGAGTGGGTTGGGTTGCCAGATC 1260
Qy 1382 AAGTTGCACTTGGTGCACCAAGAAACGGGAGGAGCCCTTCTTCGAGGAGAGGAC 1441
Db 1261 AAGTTGCACTTGGTGCACCAAGAAACGGGAGGAGCCCTTCTTCGAGGAGAGGAC 1320
Qy 1442 TGCAGCGTGTGAGGTGACAGAGGGAGGTTAAGAACTCAGTCAGGCTCATCCCCAGC 1501
Db 1321 TGCAGCGTGTGAGGTGACAGAGGGAGGTTAAGAACTCAGTCAGGCTCATCCCCAGC 1380
Qy 1502 TGGACACGGTGATCCTGCTGAAGTCCATGTGTGAGGAAGCGTTCCTTTGGGAAACCCGTT 1561
Db 1381 TGGACACCGTGATCCTGCTGAAGTCCATGTGTGAGGAAGCGTTCCTTTGGGAAACCCGTT 1440
Qy 1562 GAGCCCCAGGCAAGGAGGAAAGAGCGATCCATGTCTGCTCCAGGAAACCTACTGGTGAA 1621
Db 1441 GAGCCCCAAGCAAGGAGGAAAGAGCGATCCATGTCTGCTCCAGGAAACCTACTGGTGAA 1500
Qy 1622 GAAGGTTTGTGAGAGGGGCAAGAGCCAGAGCTCCCGGCGTCCAGGAGAGGAGCT 1681
Db 1501 GAAGGTTTGTGAGAGGGGCAAGAGCCAGAGCTCCCGGCGTCCAGGAGAGGAGCT 1560
Qy 1682 GCATCCTGAGCCCTGCATGACCCAGGCGCAACCCGCGAGACACTCATCC 1732
Db 1561 GCATCCTGAGCCCTGCATGACCCAGGCGCAACCCGCGAGACACTCATCC 1611

RESULT 7

ABX97034

ID ABX97034 standard; cDNA; 1547 BP.

AC ABX97034;

XX ABX97034;

DT 20-MAY-2003 (first entry)

DE Human NOV15a cDNA.

XX NOVX; cytostatic; cardiant; antiarteriosclerotic; antiasthmatic; cancer;

KW hypotensive; cardiomyopathy; bronchial asthma; gene therapy; vaccine;

XX human; gene; ss.

XX

OS Homo sapiens.
XX WO200272757-A2.
XX 19-SEP-2002.
XX 08-MAR-2002; 2002WO-US006908.
PF 08-MAR-2001; 2001US-0274101P.
XX 08-MAR-2001; 2001US-0274194P.
PR 08-MAR-2001; 2001US-0274281P.
PR 08-MAR-2001; 2001US-0274322P.
PR 09-MAR-2001; 2001US-0274849P.
PR 12-MAR-2001; 2001US-0275235P.
PR 13-MAR-2001; 2001US-0275578P.
PR 13-MAR-2001; 2001US-0275579P.
PR 13-MAR-2001; 2001US-0275601P.
PR 14-MAR-2001; 2001US-0276000P.
PR 16-MAR-2001; 2001US-0276776P.
PR 19-MAR-2001; 2001US-0276994P.
PR 20-MAR-2001; 2001US-0277239P.
PR 20-MAR-2001; 2001US-0277321P.
PR 20-MAR-2001; 2001US-0277327P.
PR 21-MAR-2001; 2001US-0277791P.
PR 22-MAR-2001; 2001US-0277833P.
PR 23-MAR-2001; 2001US-0278152P.
PR 26-MAR-2001; 2001US-0278894P.
PR 27-MAR-2001; 2001US-0278999P.
PR 27-MAR-2001; 2001US-0279036P.
PR 28-MAR-2001; 2001US-0279344P.
PR 30-MAR-2001; 2001US-0277338P.
PR 30-MAR-2001; 2001US-0279995P.
PR 30-MAR-2001; 2001US-0280233P.
PR 02-APR-2001; 2001US-0280802P.
PR 02-APR-2001; 2001US-0280822P.
PR 02-APR-2001; 2001US-0280900P.
PR 04-APR-2001; 2001US-0281194P.
PR 13-APR-2001; 2001US-0283675P.
PR 30-APR-2001; 2001US-0287424P.
PR 02-MAY-2001; 2001US-0288066P.
PR 03-MAY-2001; 2001US-0288342P.
PR 03-MAY-2001; 2001US-0288528P.
PR 15-MAY-2001; 2001US-0291190P.
PR 16-MAY-2001; 2001US-0291099P.
PR 16-MAY-2001; 2001US-0291240P.
PR 30-MAY-2001; 2001US-0294485P.
PR 31-MAY-2001; 2001US-0294889P.
PR 31-MAY-2001; 2001US-0294899P.
PR 18-JUN-2001; 2001US-0299027P.
PR 19-JUN-2001; 2001US-0299303P.
PR 19-JUN-2001; 2001US-0299310P.
PR 10-JUL-2001; 2001US-0304354P.
PR 31-JUL-2001; 2001US-0309198P.
PR 16-AUG-2001; 2001US-0312903P.
PR 10-SEP-2001; 2001US-0318462P.
PR 12-SEP-2001; 2001US-0318770P.
PR 27-SEP-2001; 2001US-0325430P.
PR 27-SEP-2001; 2001US-0325681P.
PR 18-OCT-2001; 2001US-0330380P.
PR 31-OCT-2001; 2001US-0335301P.
PR 14-NOV-2001; 2001US-0332172P.
PR 14-NOV-2001; 2001US-0332271P.
PR 14-NOV-2001; 2001US-0332272P.
PR 14-NOV-2001; 2001US-0333184P.
PR 21-NOV-2001; 2001US-0332094P.
PR 03-DEC-2001; 2001US-0337426P.
PR 03-DEC-2001; 2001US-0338092P.
PR 04-DEC-2001; 2001US-0337185P.
PR 03-JAN-2002; 2002US-0345705P.
PR 07-MAR-2002; 2002US-00092900.
XX (CURA-) CURAGEN CORP.
XX PA

[illegible]

QY 542 CAGCTGAACCACTACAGCTGCGAGTGAATGGCAAGGGTGCCTACCGTGTGTGAGG 601
Db 421 CAGCTGAACCACTACAGCTGCGAGTGAATGGCAAGGGTGCCTACCGTGTGTGAGG 480
QY 602 CTGGCCCTACAAACCAAGTGAAGACGACACTATGCAATGAAGTCTCTTTCCAAAAGAAG 661
Db 481 CTGGCCCTACAAACCAAGTGAAGACGACACTATGCAATGAAGTCTCTTTCCAAAAGAAG 540
QY 662 TTACTGAAGCAGTATGCTTTTCAACGTCGCTTCCCTCCCGAGAGGGTCCAGGCTGCCAG 721
Db 541 TTACTGAAGCAGTATGCTTTTCAACGTCGCTTCCCTCCCGAGAGGGTCCAGGCTGCCAG 600
QY 722 GGAGGACCGCCAGCAGCTGCTGCCCTCCCTGGAGGGGTGTACAGAGATTGCAATCCTG 781
Db 601 GGAGGACCGCCAGCAGCTGCTGCCCTCCCTGGAGGGGTGTACAGAGATTGCAATCCTG 660
QY 782 AAGAAGCTGGACCACTGAAATGGGTCAAACTGATCGAGGTCTGTGATGACCCAGCTGAG 841
Db 661 AAGAAGCTGGACCACTGAAATGGGTCAAACTGATCGAGGTCTGTGATGACCCAGCTGAG 720
QY 842 GACAACTCTAATTTG----- 856
Db 721 GACAACTCTAATTTG----- 856
QY 857 ----- 856
Db 781 ATGCCCAAGTCCCACTCCCTGCTTCCCTGTGACGACGAAGACAGTGGATCCAGTGGCT 840
QY 857 -----GTGTTTGACCTCTCTGAGAAAGGGCCCGTCTATGAAAGTGCCTCTGTACAAG 907
Db 841 GCGCGCTCAGTGTGTTGACCTCTCTGAGAAAGGGCCCGTCTATGAAAGTGCCTGTGACAAG 900
QY 908 CCTTCTCGAGGAGCAAGCTGCCTCTACTCTCGGAGCGTCACTCTGGGCTCTCGAGTAC 967
Db 901 CCTTCTCGAGGAGCAAGCTGCCTCTACTCTCGGAGCGTCACTCTGGGCTCTCGAGTAC 960
QY 968 TTGCACTGCCAGAGATCGTCCACAGGACATCAAGCCATCCAACTGCTCTCTGGGGAT 1027
Db 961 TTGCACTGCCAGAGATCGTCCACAGGACATCAAGCCATCCAACTGCTCTCTGGGGAT 1020
QY 1028 GATGGCAGCTGAAGATCGCCGCTTTGGGCTCAGCAACCAAGTTTGAGGGGAACGACGCT 1087
Db 1021 GATGGCAGCTGAAGATCGCCGCTTTGGGCTCAGCAACCAAGTTTGAGGGGAACGACGCT 1080
QY 1088 CAGCTTCAGCAACGCGGGAACCCAGCAATTCATGGCCCGCAGGCCAATTTCTGATTC 1147
Db 1081 CAGCTTCAGCAACGCGGGAACCCAGCAATTCATGGCCCGCAGGCCAATTTCTGATTC 1140
QY 1148 GCGCAGCTTCAGTGGGAAGGCTTGGATGTATGGGCCACTGGCGTCAGTTGTACTGC 1207
Db 1141 GCGCAGCTTCAGTGGGAAGGCTTGGATGTATGGGCCACTGGCGTCAGTTGTACTGC 1200
QY 1208 TTTGTCATATGGGAAGTGCCTTCATCGACGATTCATCTGGCCCTCCACAGGAAGATC 1267
Db 1201 TTTGTCATATGGGAAGTGCCTTCATCGACGATTCATCTGGCCCTCCACAGGAAGATC 1260
QY 1268 AGAATGAGCCCGTGTGTTTCTGAGGAGCCAGAAATCAGCAGAGCTCAAGGACCTG 1327
Db 1261 AGAATGAGCCCGTGTGTTTCTGAGGAGCCAGAAATCAGCAGAGCTCAAGGACCTG 1320
QY 1328 ATCCTGAAGATTAGACAGATCCGAGACGAAATGGGTGCGCAGACATCAAGTTG 1387
Db 1321 ATCCTGAAGATTAGACAGAAATCCGAGACGAAATGGGTGCGCAGACATCAAGTTG 1380
QY 1388 CACCTTTGGTGTACCAAGACGGGAGGAGCCCTCTCTTCGAGGAGGAGCACTGCAGC 1447
Db 1381 CACCTTTGGTGTACCAAGACGGGAGGAGCCCTCTCTTCGAGGAGGAGCACTGCAGC 1440
QY 1448 GTGGTGAAGTGCAGAGGGGGAGGTTAAGAACTCAGTACAGGCTCATCCCGAGCTGACC 1507
Db 1441 GTGGTGAAGTGCAGAGGGAGGAGGTTAAGAACTCAGTACAGGCTCATCCCGAGCTGACC 1500
QY 1508 ACGTGTATCCTGTGAAGTCCATGTCTGAGGAAGCGTTCCTTTGGGAACCGCTTTGAGCC 1567

Db 1501 ACGTGTATCCTGTGAAGTCCATGTCTGAGGAAGCGTTCCTTTGGGAACCGCTTTGAGCC 1560
QY 1568 CAGGACCGAGGGAAGAGGATCCATGTCTGTCTCCAGGAAACCTACTGTGTGAAGAAGGG 1627
Db 1561 CAAGCAAGGGAAGAGGATCCATGTCTGTCTCCAGGAAACCTACTGTGTGAAGAAGGG 1620
QY 1628 TTTGTGTGAAGGGGGCAAGAGCCAGAGCTCCCGCGCTCCAGGAAGCAGAGGCTGCATCC 1687
Db 1621 TTTGTGTGAAGGGGGCAAGAGCCAGAGCTCCCGCGCTCCAGGAAGCAGAGGCTGCATCC 1680
QY 1688 TGAGCCCTGTGATGCAACCCAGGCGCACCCGGGAGCACATCATCC 1732
Db 1681 TGAGCCCTGTGATGCAACCCAGGCGCACCCGGGAGCACATCATCC 1725

RESULT 9
AAS06710
ID AAS06710 standard; cDNA; 1542 BP.
XX
AC AAS06710;
XX AC
XX 12-SEP-2001 (first entry)
XX
DE Polynucleotide sequence encoding human protein kinase #10.
XX
KW Human; protein kinase; PTK; STK; cancer; cardiovascular disease;
KW metabolic disorder; immune related disease; neurological disorder;
KW neurodegenerative disorder; inflammatory disorder; infectious disease;
KW reproductive disorder; gene therapy; ss.
XX
OS Homo sapiens.
XX
PN WO200138503-A2.
XX
PD 31-MAY-2001.
XX
PF 22-NOV-2000; 2000WO-US032085.
XX
PR 24-NOV-1999; 99US-0167482P.
XX
XX (SUGEN-) SUGEN INC.
XX
PI Plowman GD, Whyte D, Manning G, Sudarsanam S, Martinez R;
PI Flanagan P, Clary D;
XX
XX WPI; 2001-343950/36.
DR P-PSDB; AAU03510.
XX
XX Nucleic acids encoding human kinase polypeptides, useful for preventing
PT diagnosing and/or treating e.g. cancer, immune, cardiovascular and
PT neuronal-associated diseases, and microbial infections.
XX
XX Example 1; Fig 1; 433pp; English.
XX
CC AAS06701-AAS06757 encode for novel human protein kinases #1-57. The novel
CC protein kinases have been identified as members of the tyrosine or
CC serine/threonine kinase (PTK and STK) families. The polynucleotides
CC encoding protein kinases and the polypeptides may be used in the
CC prevention, diagnosis and treatment of diseases associated with
CC inappropriate kinase expression. For example, they may be used to treat
CC cancers (especially cancers of haematopoietic origin), cardiovascular
CC disease (e.g. atherosclerosis), metabolic disorders (e.g. diabetes),
CC immune related diseases (e.g. rheumatoid arthritis), neurological
CC disorders (e.g. schizophrenia), neurodegenerative disorders (e.g.
CC Parkinson's disease), inflammatory disorders (e.g. asthma), infectious
CC disease (e.g. HIV) and reproductive disorders (e.g. infertility).
CC Additionally, polynucleotides encoding protein kinases may be used for
CC gene therapy and as DNA probes in diagnostic assays. The protein kinase
CC polypeptides may be used as antigens in the production of antibodies
CC against the protein kinases and in assays to identify modulators of
CC protein kinase expression and activity

SQ	Sequence	1542 BP; 349 A; 428 C; 483 G; 282 T; 0 U; 0 Other;
Query Match	66.7%; Score 1461.8; DB 4; Length 1542;	
Best Local Similarity	97.9%; Pred. NO. 1.1e-307;	
Matches 1513; Conservative	0; Mismatches 2; Indels 30; Gaps 2;	
QY	173 ATGAGGGGGTCCAGCTGTCTGCTCCAGGATCCTCGGCAGAGCTGGTAGACGGGTG	232
DB	1 ATGAGGGGGTCCAGCTGTCTGCTCCAGGATCCTCGGCAGAGCTGGTAGACGGGTG	60
QY	233 GCAGCCATCGATGTGACTCACTTGGAGGAGGAGATGGTGGCCAGAGCCTACTAGAAAC	292
DB	61 GCAGCCATCGATGTGACTCACTTGGAGGAGGAGATGGTGGCCAGAGCCTACTAGAAAC	120
QY	293 GGTGTGACCCGCCACACAGGGCCAGAGCTGCTGTGTATGCCCTGGCAGTACTTCAAGA	352
DB	121 GGTGTGACCCGCCACACAGGGCCAGAGCTGCTGTGTATGCCCTGGCAGTACTTCAAGA	180
QY	353 CTGCTCCAGCCCGGCTAGCCTCTCAGCCAGGAAGCTTTCCTACAGAGCGGCCAGCA	412
DB	181 CTGCTCCAGCCCGGCTAGCCTCTCAGCCAGGAAGCTTTCCTACAGAGCGGCCAGCA	240
QY	413 GGAAGCTATCTGGAGCGCAGGCTGGGCTTTATGCCAGGGGCTTGCAGCCACATCTCC	472
DB	241 GGAAGCTATCTGGAGCGCAGGCTGGGCTTTATGCCAGGGGCTTGCAGCCACATCTCC	300
QY	473 CCCCAGGCTGGCGAGGCGCCACCATCGAGTCCACACGCTGGCCATCTCAGATGCAG	532
DB	301 CCCCAGGCTGGCGAGGCGCCACCATCGAGTCCACACGCTGGCCATCTCAGATGCAG	360
QY	533 GACTGCTGTCAGCTGAACCAAGTACAGTGCAGAGTGAGATTGGCA-----	578
DB	361 GACTGCTGTCAGCTGAACCAAGTACAGTGCAGAGTGAGATTGGCA-----	420
QY	579 -----AGGGTCCCTACGCTGTGTGGCTGGCTTACCAAGAGTGGCTTTTCCA	625
DB	421 GATGCTTATCTGCAGGGTGCCTTACGCTGTGTGGCTGGCTTACCAAGAGTGGCTTTTCCA	480
QY	626 AGACATATGCAATCAAGTCTTTTCCAAAGAGTACTTGMAGCAGTATGGCTTTTCCA	685
DB	481 AGACATATGCAATCAAGTCTTTTCCAAAGAGTACTTGMAGCAGTATGGCTTTTCCA	540
QY	686 CGTCCCTCTCCCGGAGGGGTCCAGGCTGCCAGGGAGGACCAAGCAAGCAGCTGCTG	745
DB	541 CGTCCCTCTCCCGGAGGGGTCCAGGCTGCCAGGGAGGACCAAGCAAGCAGCTGCTG	600
QY	746 CCCCTGGAGCGGGTGTACAGAGATGCCATCTCTGAAGAGCTGGACACGTAATGTG	805
DB	601 CCCCTGGAGCGGGTGTACAGAGATGCCATCTCTGAAGAGCTGGACACGTAATGTG	660
QY	806 GTCBAACCTGATCGAGTCTGTGATGACCCAGCTGAGGACACCTCTATTGGTGTTCAC	865
DB	661 GTCBAACCTGATCGAGTCTGTGATGACCCAGCTGAGGACACCTCTATTGGTGTTCAC	717
QY	866 CTCCTTGAGAAAGGGCCCGCTCATGGAAGTGCCTGTGACAAAGCCCTTCTCGAGAGGACAA	925
DB	718 CTCCTTGAGAAAGGGCCCGCTCATGGAAGTGCCTGTGACAAAGCCCTTCTCGAGAGGACAA	777
QY	926 GCTCGCCTCTACCTCGGGAGAGTCACTCTGGGCTCGAGTACTTTCACCTGCAGAGATC	985
DB	778 GCTCGCCTCTACCTCGGGAGAGTCACTCTGGGCTCGAGTACTTTCACCTGCAGAGATC	837
QY	986 GTCCACAGGGACATCAAGCCATCCAACTGCTCTCTGGGGGATGATGGGCAGCTGAAGATC	1045
DB	838 GTCCACAGGGACATCAAGCCATCCAACTGCTCTCTGGGGGATGATGGGCAGCTGAAGATC	897
QY	1046 GCCGACTTTGGCGTTCAGCAACAGTTTTCAGGGGACAGCGCTCAGCTGTCCAGCACGCG	1105
DB	898 GCCGACTTTGGCGTTCAGCAACAGTTTTCAGGGGACAGCGCTCAGCTGTCCAGCACGCG	957
QY	1106 GGAAACCCAGGATTCATGCCCCCGAGGCCATTTCTGATTCGGGCCAGAGCTTCAGTGGG	1165
DB	958 GGAAACCCAGGATTCATGCCCCCGAGGCCATTTCTGATTCGGGCCAGAGCTTCAGTGGG	1017

QY	1166 AAGGCTTGGATGTATGGGCCACTGGCGTCACTTGTACTGCTTTGTCTATGGGAAGTGC	1225
DB	1018 AAGGCTTGGATGTATGGGCCACTGGCGTCACTTGTACTGCTTTGTCTATGGGAAGTGC	1077
QY	1226 CCATTTCATCGACGATTTTCATCCTGGCCCTCCACAGGAAGATCAAGAAATGAGCCCGTGGTG	1285
DB	1078 CCATTTCATCGACGATTTTCATCCTGGCCCTCCACAGGAAGATCAAGAAATGAGCCCGTGGTG	1137
QY	1286 TTTCTGAGGAGCCAGAAATCAGCGAGGAGTCAAGGACCTGATCCTGAAGATGTTAGAC	1345
DB	1138 TTTCTGAGGAGCCAGAAATCAGCGAGGAGTCAAGGACCTGATCCTGAAGATGTTAGAC	1197
QY	1346 AAGATCCCGAGAGAGNAATTGGGGTGCACACATCAAGTTGCACCCCTTGGGTGACCAAG	1405
DB	1198 AAGATCCCGAGAGAGNAATTGGGGTGCACACATCAAGTTGCACCCCTTGGGTGACCAAG	1257
QY	1406 AACGGGAGGAGCCCTTTCCTTCGGAGGAGGAGCACTGCAGCGTGGTGGAGTGCACAG	1465
DB	1258 AACGGGAGGAGCCCTTTCCTTCGGAGGAGGAGCACTGCAGCGTGGTGGAGTGCACAG	1317
QY	1466 GGGAGAGTTAAGAACTCAGTCAGGCTCATCCCGAGCTGGACACAGTGTATCCTGGTGAAG	1525
DB	1318 GAGGAGGTTAAGAACTCAGTCAGGCTCATCCCGAGCTGGACACAGTGTATCCTGGTGAAG	1377
QY	1526 TCCATGCTGAGGAAGCGTTCTTTGGGAAACCCGTTTGAGCCCCCAGGACGGAGGAAG	1585
DB	1378 TCCATGCTGAGGAAGCGTTCTTTGGGAAACCCGTTTGAGCCCCCAGGACGGAGGAAG	1437
QY	1586 CGATCCATGCTGCTCCAGGAAACCTACTGCTGAAAGAGGGTTTGGTGAAGGGGGCAAG	1645
DB	1438 CGATCCATGCTGCTCCAGGAAACCTACTGCTGAAAGAGGGTTTGGTGAAGGGGGCAAG	1497
QY	1646 AGCCAGAGCTCCCCGGGCTCCAGGAAGACGAGGCTGCATCTCTGA	1690
DB	1498 AGCCAGAGCTCCCCGGGCTCCAGGAAGACGAGGCTGCATCTCTGA	1542
RESULT 10		
ADB53308		
ID	ADB53308 standard; DNA; 3411 BP.	
XX	ADB53308;	
XX	ADB53308;	
DT	04-DEC-2003 (first entry)	
XX		
DE	Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:3850.	
XX		
KW	toxic effect; gene expression profile; hepatotoxicity; diagnostic marker;	
KW	toxicity marker; toxicity progression; drug screening;	
KW	primary rat hepatocyte toxicity modelling; gene; ds.	
XX		
OS	Rattus norvegicus.	
XX		
PN	WO2003065993-A2.	
XX		
PD	14-AUG-2003.	
XX		
PF	04-FEB-2003; 2003WO-US003482.	
XX		
PR	04-FEB-2002; 2002US-0353171P.	
PR	13-MAR-2002; 2002US-0363534P.	
PR	08-APR-2002; 2002US-0370248P.	
PR	10-APR-2002; 2002US-0371134P.	
PR	10-APR-2002; 2002US-0371135P.	
PR	10-APR-2002; 2002US-0371150P.	
PR	11-APR-2002; 2002US-0371413P.	
PR	19-APR-2002; 2002US-0373601P.	
PR	22-APR-2002; 2002US-0374139P.	
PR	08-MAY-2002; 2002US-0378370P.	
PR	09-MAY-2002; 2002US-0378652P.	
PR	09-MAY-2002; 2002US-0378653P.	

Db 1552 GAAAGAGGATGTGAGAGGGGGGCAAAAGCCAGAGCTTCCGGAGTCCAGGAAGATGA 1611
Qy 1678 GGCTGATCTGAGCCCTGATGACCCAGGGCCACCCGGCAGACACTCATCCCGCGC 1737
Db 1612 GGCTGATCTGAGTCCCTGATGTCGCGCCAGGGCCA-TGGGAGCATGCTCATTCGGCTC 1670
Qy 1738 CTCAGAGGCCAC--CCCTCATGCAACAGCGGCCCGCCAGGCGAGGGGCTGGGGACTG 1795
Db 1671 CTCAGAGGCCACCGCCCTCATGCAATCATGCGCCCTGCAAGGCAGGGGCTGGGGACTG 1730
Qy 1796 CAGCCCCACTCC---CGCCCCCTCCCGCATCGTGTGCAATGACCTCCACGCGACGCACTCC 1852
Db 1731 CAGCCCCCTCTCTGCCCCCTCCACCGAATGTCGTGATGACCTGCGGACAGGCATATCC 1790
Qy 1853 AGGACACA-GACTGGGAATGATGTATTTGGGGTCTTTGGGGGAGGGCT 1899
Db 1791 AGGACAGGATTGGAATGTATCATTTGGGGCTCGGGGCTCCCGGTT 1838

RESULT 11

AZ29223
ID AZ29223 standard; cDNA; 2545 BP.

XX AC AZ29223;

XX DT 28-FEB-2000 (first entry)

XX DE Human cell signalling protein-2 encoding cDNA.

XX DE Cell signalling protein-2; CSIGP-2; cell proliferation; arteriosclerosis;
KW inflammatory disorder; cirrhosis; cancer; hepatitis; AIDS;
KW Addison's disease; multiple sclerosis; ss.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers
XX CDS 241..1860
FT /*tag= a
FT /product= "Cell Signalling Protein-2"

XX WO9958558-A2.

XX PD 18-NOV-1999.

XX DF 13-MAY-1999; 99WO-US010567.

XX PR 13-MAY-1998; 98US-0085343P.

XX PR 26-AUG-1998; 98US-0098010P.

XX XX (INCY-) INCYTE PHARM INC.

XX PI Bandman O, Hillman JL, Lal P, Yue H, Tang YT, Patterson C;
XX PI Baughn MR, Yang J;

XX DR WPI; 2000-086432/07.

XX DR P-PSDB; AAY44239.

XX PT Human cell signaling proteins useful for, e.g. diagnosing cell
XX PT proliferative and inflammatory disorders.

XX PS Claim 9; Page 80-81; 90pp; English.

XX CC The present sequence is a cDNA obtained from Incyte clone 640521 of
XX CC BRSTN03 library. It encodes cell signalling protein-2 (CSIGP-2). It is
XX CC expressed in reproductive, nervous and developmental tissues. Fragments
XX CC of CSIGP encoding nucleic acid can be used as hybridisation probe for
XX CC detecting CSIGP related sequences or allelic variants. Recombinant CSIGP
XX CC can be produced in host cells by transforming them with genetically
XX CC engineered vectors. Agonists or antagonists can be used in the treatment
XX CC of cell proliferative and inflammatory disorders associated with
XX CC decreased or increased CSIGP expression. CSIGP is used in the diagnosis,
XX CC prevention and treatment of cell proliferative disorders like

CC arteriosclerosis, cirrhosis, cancer, hepatitis and inflammatory disorders
CC like AIDS, Addison's disease, multiple sclerosis, etc
XX SQ Sequence 2545 BP; 542 A; 737 C; 760 G; 506 T; 0 U; 0 Other;
Query Match 30.2%; Score 661; DB 3; Length 2545;
Best Local Similarity 71.0%; Pred. No. 1.1e-133;
Matches 890; Conservative 0; Mismatches 360; Indels 3; Gaps 1;
Qy 439 GCCTTATGCCAGGGGCTGCCAGCCACATCTCCCGGAGCTTCCCGGAGTCCAGGAAGATGA 1611
Db 618 GCCCTACTACCCCTGAGTCCCGCAGTCTCGCTCGGCTGCGCCGCGCGCCGACAGT 677
Qy 499 CGAGTCCCACCACTGGGCCATCTCAGATGCAGAGGAGTGGTGCAGCTGAACCACTGACAA 558
Db 678 GGAGTCTCACCACGCTCTCCATCAGGGGTATCAGGAGTGTGTGAGCTGAATCAGATATAC 737
Qy 559 GCTGCAGAGTGAAGTTGGCAAGGGTCTACGGGTGTGTGAGGGTGGCTTCAACGAAAG 618
Db 738 CCTGAAGGATGAATTGGAAAGGCTCTATGGTGTCTCAAGTTGGCTTCAATGAAGA 797
Qy 619 TGAAGACAGACACTATGCAATGAAGTCTTTTCCAAAAGAAAGTTACTGAAGCAGTATGG 678
Db 798 TGACAAATACCTACTATGCAATGAAGTCTGTCCAAAAGAAAGTGTATCCGCGAGCCGG 857
Qy 679 CTTTCCAGCTGCGCCCTCCCGAGAGGGTCCCGAGCTGCCAGGAGGACCGACCAAGCA 738
Db 858 CTTTCCAGCTGCGCCCTCCCGAGGACCCCGGAGCTCTCTGGAGGCTGCATCCAGCC 917
Qy 739 GCTGTGCTCCCTGGAGGGGTGTACAGGAGATGCCATCTCTGAAGAGCTGGACCACT 798
Db 918 CAGGGGCCCATTCAGCAGGTGTACACAGGAATGCCATCTCAAGAAAGCTGGACCACT 977
Qy 799 GAATGTGTCAAACTGATCGAGGTCTCTGGATGACCCAGCTGAGGACCACTTATTTGGT 858
Db 978 CAATGTGTGAAGCTGTGGAGTCTCTGGATGACCCCAATGAGGACCACTTGTATCATG 1037
Qy 859 GTTTGACCTCTGAGAAAGGGGCGCTCATGMAAGTGCCCTGTGACAAAGCCCTTCTCGGA 918
Db 1038 GTTTCGACTGGTCAACGAGGCGCGTGTGAGAGTGGCCACCTTCAACCACTCTCTGA 1097
Qy 919 GGAGCAAGCTCGCTCTACTCTGCGGAGCTCATCTGGGCTCTGAGTACTTGCATGCCA 978
Db 1098 AGACGAGCGCGTTTCTACTTCCAGGATCTGATCAAGGGCATCGAGTACTTACACTACA 1157
Qy 979 GAAGATCGTCCAGGGACATCAAGCCATCAACCTCTCTGGGGAGTATGGGAGT 1038
Db 1158 GAAGATCATCCACCGTGCATCAACCTCTCTGAGAGGAGTGGGAGT 1217
Qy 1039 GAAGATCGCGACTTTGGCGTCAAGCAAGCTTTGAGGGGAAAGAGCTCTGCTCCAG 1098
Db 1218 CAGATCGCTGACTTTGGTGTGAGCAATGAATCAAGGGCAGTGAAGCTCTCTCCAA 1277
Qy 1099 CACGGCGGAAACCCAGCATTTATGGCCCCCGAGGCAATTTCTGATTCGGGCAAGCTT 1158
Db 1278 CACCGTGGGACGCGCGCTTTCATGGCACCAGCTGCTCTCTGAGACCGCAAGATCTT 1337
Qy 1159 CAGTGGGAGGCTTGGATGTATGGGCCACTGGGCTGAGTGTACTGTCTTGTCTATGG 1218
Db 1338 CTCTGGGAGGCGCTTGGATGTTTGGGCTATGGGTGTGACATATCTCTTGTCTTGG 1397
Qy 1219 GAAGTGCCCATTCATCGACGATTTTCATCTCGGCCCTCCACAGGAGATCAAGAAATGAGCC 1278
Db 1398 CCAGTGCCCATTCATGGACGAGCGGATCATGTGTTACAGTAAAGTCAAGAGTCAGGC 1457
Qy 1279 CGTGGTGTTCCTGAGGAGCAGAAAATCAGGAGGAGCTCAAGGACCTGATCTCTGAAGAT 1338
Db 1458 CTTGGAATTTCCAGACCCAGCCGACATAGCTGAGGACTTGAAGGACCTGATCACCGTAT 1517
Qy 1339 GTTAGACAAGAAATCCGAGACGAGAAATTTGGGGTGCAGACATCAAGTTGCACCTTGGT 1398
Db 1518 GCTGGAAGAAGACCCCGAGTCTGAGATCGTGTGCGGAATCAAGCTGCACCCCTGGT 1577

QY 1399 GACCAAGAACGGGAGGAGCCCTTCTTCGAGAGGAGCACTGCAGCGTGGTGAAGT 1458
XX |||||
Db 1578 CACGAGGATGGGGGAGCCGTTCGCTCGAGGATGAGAACTGCACGCTGGTGAAGT 1637
QY 1459 GNCAGAGGGGAGGTTAGAACTCAGTCAGGCTCATCCCGAGCTGCACCGTGAATCCT 1518
XX |||||
Db 1638 GACTGAAGAGGAGGTCGAGAACTCAGTCAAAACATTTCCAGCTTGGCAACCGTGAATCT 1697
QY 1519 GGTGAAGTCCATGCTGAGGAAGCGTTTCTTTGGGAACCGGTTTGAGCCCGCAGGACGGAG 1578
XX |||||
Db 1698 GGTGAAGACCATGATAGTAAAGCTCTCTTTGGGAACCATTCGAGGC--AGCGGGG 1754
QY 1579 GGAAGAGCGATCATGCTGCTCCAGGAAACCTATCTGGTGAAGAGGTTGGTGAAGG 1638
XX |||||
Db 1755 GGAGGAACCTCACTGTCAGCGCTCGAACTTGCTCAGGAAGCAAGGAGGAGGAGCAAA 1814
QY 1639 GGGCAGAGCCAGAGCTCCCGGCTGCAGGAAGAGGAGGCTGCATCTGAG 1691
XX |||||
Db 1815 CCTCAGGAGCAGCAGCCCGCCCGCTGGGGAGGAGGAAGTCTCTTGTGAG 1867

RESULT 12

ID ADB75227 standard; cDNA; 4942 BP.

AC ADB75227;

DT 04-DEC-2003 (first entry)

DE Prostate cancer marker cDNA.

XX Prostate; cancer; cytostatic; gene therapy; marker; ss.

XX Homo sapiens.

OS WO2003009814-A2.

XX 06-FEB-2003.

PF 25-JUL-2002; 2002WO-US023913.

XX 25-JUL-2001; 2001US-0307982P.

PR 22-AUG-2001; 2001US-0314356P.

PR 25-SEP-2001; 2001US-0325020P.

PR 12-DEC-2001; 2001US-0341746P.

PR 05-MAR-2002; 2002US-0362158P.

XX (MILL-) MILLENNIUM PHARM INC.

XX Schlegel R, Monahan JE, Endege WO, Gamnavarapu M, Gorbacheva B;

PI Hoerh S, Kamatkar S, Wonsey AM, Glatt X, Zhao X, Anderson D;

XX WPI; 2003-248033/24.

XX New nucleic acid molecule, useful for diagnosing or treating prostate

PT cancer.

XX Claim 1; SEQ ID NO 51; 99pp; English.

XX The invention relates to newly discovered cancer markers associated with
CC the cancerous state of prostate cells. Also disclosed is a method of
CC assessing whether a patient is afflicted with prostate cancer. The method
CC of the invention involves assessing whether a patient is afflicted with
CC prostate cancer by comparing the level of expression of a marker in a
CC patient sample and the normal level of expression of the marker in a
CC control non-prostate cancer sample, where a significant increase in the
CC level of expression of the marker in the patient sample and the normal
CC level indicates that the patient is afflicted with prostate cancer.
CC Nucleic acids of the invention are useful for diagnosing or treating
CC prostate cancer, and may be useful in gene therapy. Sequences given in
CC ADB75177-ADB75631 represent marker cDNA and proteins. Note: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format directly from WIPO at

CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 4942 BP; 1169 A; 1294 C; 1356 G; 1122 T; 0 U; 1 Other;
Query Match 29.7%; Score 651.2; DB 9; Length 4942;
Best Local Similarity 71.3%; Pred. No. 1.7e-131;
Matches 873; Conservative 0; Mismatches 348; Indels 3; Gaps 1;
QY 439 GCCTTATGTCACGGGCGCTGCCAGGCACATCTCCCGCGGCTGGCGGAGGCCACCAT 498
XX |||||
Db 536 GCCTTACTCACCGTCAGCTCCCGCAGTCTCGCTCGCTGCCCGCGCGCAGACGT 595
QY 499 CGAGTCCCACACGTCGTCAGTTCAGATGCAGAGACTCGTCGTCGAGCTGAACACGATCAA 558
XX |||||
Db 596 GGAGTCTCACACGTCCTCATCAGGGTATGAGGACTGTGTGCGACTGAATCAGTATAC 655
QY 559 GCTGCAGAGTGAATTTGGCAAGGGTCCCTACGCTGTGGTGGAGCTGGCCCTCAACCGAAG 618
XX |||||
Db 656 CTGAAGGATGAAATTTGAAAGGGTCTCTATGCTGCTCAAGTTGGCCCTCAATGAAA 715
QY 619 TGAAGACAGACACTATGCAATGAAAGTCTCTTCCAAAAGAAAGTTACTGAAGCAGTATGG 678
XX |||||
Db 716 TGACAATACCTACTATGCAATGAAGTCTGTCTCCAAAAGAAAGTGTATCCGCGCAGCGG 775
QY 679 CTTTCCAGCTCGCCCTCCCGAGAGGGTCCAGGCTGCCAGGAGGAGGACCGACCAAGCA 738
XX |||||
Db 776 CTTTCCAGCTCGCCCTCCACCGCAGGACCCCGGCGAGCTCTCTGGAGGGTGCATCCAGCC 835
QY 739 GCTGCTGCCCTGGAGCGGCTGTACCAGGAGATTCGCTATCTTGAAGAACTGCACCACT 798
XX |||||
Db 836 CAGGGGCCCATTTGAGCAGGTGTACAGGAATTTGCCATCTCCAGAACTGGACCAACC 895
QY 799 GAATGTGTCAAACCTGATCAGGTCCTGGATGACCCAGCTGAGGACAACTCTATTGGT 858
XX |||||
Db 896 CAATGTGTGAAGTGTGTGAGTCTCTGATGACCCCAATGAGGACCACTCTGTACATGGT 955
QY 859 GTTTGACCTCTGAGAAAGGGGCGCTCATGGAAGTGCCTGTGACAAGCCCTTCTCGGA 918
XX |||||
Db 956 GTTCGAACCTGGTCAACCAAGGGCGCTGTGATGAAGTGCCTCACCCCTCAAAACCACTCTCTGA 1015
QY 919 GGAGCAAGCTCGCTCTACTCGGGAGCTGTCTCTGGGCTCGAGTACTTGCACCTGCCA 978
XX |||||
Db 1016 AGACGAGGCGGCTTCTACTTCAGGATCTGATCAAAAGGATCGAGTACTTACACTACCA 1075
QY 979 GAAGATCGTCCACAGGACATCAAGCCATCCAACTGCTCTCTGGGGGATGATGGGACGT 1038
XX |||||
Db 1076 GAAGATATCCACCGTGACATCAAACTCTTCAACCTCTCTGGTCCGAGAAGATGGGCACAT 1135
QY 1039 GAAGATCGCGGACTTTGGGCTGAGCAACAGTTTGAAGGGAAGCAGCTCAGCTGTCCAG 1098
XX |||||
Db 1136 CAAGATCGCTGACTTTGGTGTGAGCAATGAATTTCAAGGGCAGTGACGCGCTCTCTCTCAA 1195
QY 1099 CACGGGGGAACCCCGAGCATTCATGCCCGCGAGGCACTTCTGATTCGGGCGAGAGCTT 1158
XX |||||
Db 1196 CACCGTGGGCAACCGCGCTTTCATGGCACCGGAGTGCTCTCTGAGACCGCGAAGATCTT 1255
QY 1159 CAGTGGGAAGGCTTGGATGTATGGGCCACTGCGCTCACGTTGTACTGCTTGTCTATGG 1218
XX |||||
Db 1256 CTCTGGGAAGGCTTGGATGTTTGGGCCATGGTGTGACACTATATCTGCTTGTCTTGG 1315
QY 1219 GAAGTCCCATTCATCGAGATTTCTCTGGCCCTCCACAGGAAGATCAAGATGAGCC 1278
XX |||||
Db 1316 CCAGTSCCATTCATGACGAGCGGATCATGTGTTTACACAGTAAGATCAAGAGTCAAGC 1375
QY 1279 CGTGTGTTTCTCTGAGGAGCCAGAAATCAGCGAGGAGCTCAAGGACCTCATCTCTGAAGAT 1338
XX |||||
Db 1376 CTGTGAATTTCCAGACCGACCGGACATAGCTGAGGACTTGAAGGACCTGATCAACCGTAT 1435
QY 1339 GTTTAGCAAGAATTCGCCAGACGAGATTTGGGGTCCAGACATCAAGTTCACCCCTTGGGT 1398
XX |||||
Db 1436 GCTGGACAAGAACCCCGAGTCTGAGGATCTGTGGTCCGGAAATCAAGCTGCACCCCTGGGT 1495
QY 1399 GACCAAGAACGGGAGGAGGCCCTTCTTCCGGAGGAGGAGCACTGCAGCGTGTGGAGGT 1458

Db 1496 CACGAGGATGGGGGAGCGCTGCGCTCGGAGATGAGAACTGCA CGCTGGTGAAGT 1555
QY 1459 GACAGAGGGAGGTTAAGAACTGAGTCAAGGCTCATCCAGCTGGACACAGGTGATCCT 1518
Db 1556 GACTGAAGAGGAGGTCGAGAACTCACTCAAAACACATTCACAGCTTGGCAACCGTGATCCT 1615
QY 1519 GGTGAAGTCCATGCTGAGGAGCGTTCCTTTGGGAACCGGTTTGAGCCCGGACGCGAG 1578
Db 1616 GGTGAAGACCATGATACGTAAACGCTCCTTTGGGAACCCATTCGAGGGC---AGCGGCG 1672
QY 1579 GGAAGAGCGATCCATGCTGCTGCTCCAGGAAACCTACTGTTGAAAGAGGTTTGGTGAAGG 1638
Db 1673 GGAGGAACGCTCACTGTCAGCGCTGGAACCTGCTCACCAAAACCAACCAAGGAATG 1732
QY 1639 GGGCAAGAGCCAGAGCTCCCGG 1662
Db 1733 TGAGTCCCTGCTGAGCTCAAGG 1756

RESULT 13

ABK92170

ID ABK92170 standard; DNA; 1804 BP.

XX AC

XX AC

XX DT

XX 15-AUG-2002 (first entry)

XX DE

XX Prostate cancer-associated DNA sequence #56.

XX KW

XX Prostate cancer; prostate tumour tissue; human; mammal; cytostatic;

XX KW

XX gene therapy; gene; ds.

XX OS

XX Mammalia.

XX XX

XX WO200230268-A2.

XX XX

XX 18-APR-2002.

XX PD

XX 12-OCT-2001; 2001WO-US032045.

XX PF

XX 13-OCT-2000; 2000US-00687576.

XX FR

XX 08-DEC-2000; 2000US-00733288.

XX PR

XX 08-DEC-2000; 2000US-00733742.

XX PR

XX 24-JAN-2001; 2001US-0263957P.

XX PR

XX 16-MAR-2001; 2001US-0276791P.

XX PR

XX 16-MAR-2001; 2001US-0276888P.

XX PR

XX 06-APR-2001; 2001US-0281922P.

XX PR

XX 24-APR-2001; 2001US-0286214P.

XX PR

XX 30-APR-2001; 2001US-00847046.

XX PR

XX 04-MAY-2001; 2001US-0288589P.

XX XX

XX (EOSB-) BOS BIOTECHNOLOGY INC.

XX PA

XX XX

XX Gish KC, Mack DH, Wilson KE, Afar D, Hevezi P;

XX PI

XX WPI; 2002-471335/50.

XX DR

XX P-PSDB; ABG61855.

XX XX

XX PT

XX Detecting a prostate cancer-associated transcript in a cell in a patient,

XX PT useful for diagnosing prostate cancer (PC) or screening modulators of PC,

XX PT by determining if prostate cancer-associated genes are expressed in a

XX prostate tissue.

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from the tissues of various organisms such as humans or other mammals (e.g. mice, sheep and dogs). The methods of the invention are useful for diagnosing and treating prostate cancer in mammals. The prostate cancer-associated genes are useful for diagnosing or treating prostate cancer, as well as for identifying modulators of prostate cancer or agents that inhibit prostate cancer. The nucleic acid sequences are particularly useful in gene therapy, as a vaccine or in antisense applications. CC ABK92115-ABK92263 represent prostate cancer-associated polynucleotide sequences

SQ Sequence 1804 BP; 445 A; 519 C; 453 G; 387 T; 0 U; 0 Other;

Query Match 29.7%; Score 651; DB 6; Length 1804;

Best Local Similarity 71.5%; Pred. No. 1.5e-131;

Matches 871; Conservative 0; Mismatches 345; Indels 3; Gaps 1;

QY 439 GCCTTATGCCACGGGGCTGCCAGCCACATCTCCCGGCGCTGGCGGAGGCCACCAT 498

Db 30 GCCCTACTCACCGCTCAGCTCCCGCAGTCTCGCTCGCTGCCCGCGCGACAGT 89

QY 499 CGAGTCCACACCGTGGCCATCTCAGATGAGAGACTGCTGAGCTGAACCATGACAA 558

Db 90 GGAGTCTCACCGCTCTCCATCACGGGTATGACGAGCTGTGTCAGCTGAATCAGTATAC 149

QY 559 GCTGCAGAGTCAGATTGGCAAGGTCCTACGGTGTGTCAGGCTGGCTTACACGAAG 618

Db 150 CTTGAAGATGAATTTGAAAGGGCTCTATGTTGTCGTCAGTTGGCTTACATGAAAA 209

QY 619 TGAAGACAGACACTATGCAATGAAGTCTTTTCCAAAAAGATTACTGAAGAGTATGG 678

Db 210 TGCAATACCTACTATGCAATGAAGTGTCTCTCCAAAAAGAGTGTATCCGGAGCGG 269

QY 679 CTTTCCAGCTGCCCTCCCGAGAGGGTCCAGGCTGCCAGGAGGACGAGCAAGCA 738

Db 270 CTTTCCAGCTGCCCTCCCGAGGACCGCGCAGCTCTCGAGGCTGCATCCAGCC 329

QY 739 GCTGCTGCCCTCGAGGGGTGTACAGGAGATTGCCATCTGAAGAGCTGGACACGT 798

Db 330 CAGGGGCCCCATTCAGCAGGTGTACAGGAAATTTGCCATCTCAAGAGCTGGACACCC 389

QY 799 GAATGTGTCATAATGATTCGAGGTCTTGGATGACCCAGCTGAGGACACCTCTATTGGT 858

Db 390 CAATGTGTGAAGCTGTGTGGAGTCTTGGATGACCCCAATGAGGACCATCTGTACATGT 449

QY 859 GTTTGACCTCTCGAAGAGGGGCGCTCATGGAAGTGCCTGTGACAGCCCTTCTCGGA 918

Db 450 GTTCGAACTGGTCAACCAAGGGCCCGTGTGGAAGTGCCTCACCTCAACACCTCTCTGA 509

QY 919 GGAGCAAGCTCGCTCTACCTGCGGAGCTCATCTGCGGCTCGAGTACTTGCATGCGCA 978

Db 510 AGACGAGGCGGTTTCTACTTCCAGGATCTGATCAAGGCGATCGAGTACTTACACTACCA 569

QY 979 GAAGATCGTCAAGGGACATCAAGGCATCCAACTGCTCTCTGGGGATGATGGGCGAGT 1038

Db 570 GAAGATCATCCACCGTGACATCAAACTTCCAACTCTCTGGTTCGAGAGATGGGCGACAT 629

QY 1039 GAAGATCGCGACTTTGCGCTCAGCAACCACTTTGAGGGGACACGCTCAGCTGTCCAG 1098

Db 630 CAAGATCGTACTTTGTTGAGCAATGAATCAAGGGAGTGAACGCGCTCTCTCTCCAA 689

QY 1099 CACGGCGGGAACCCAGCATTTATGGCCCCCGGAGGCCATTTCTGATTTCCGGCCAGAGCTT 1158

Db 690 CACGTTGGGAGGCGCGCTTATGGCACCCGAGTGTCTCTGAGACCCGCAAGATCTT 749

QY 1159 CAGTGGGAAGCGCTTGGATGATGGGCGACTGGGCTCAGTTGTCGCTTTGTCATGG 1218

Db 750 CTCTGGGAAGGCGCTTGGATGTTGGGCGCATGGGTTGACACTATCTGCTTTGCTTTGG 809

QY 1219 GAAGTGGCCATTCATCCAGCATTTTCATCTGGGCGCTCCAGGGAAGATCAAGATGAGCC 1278

Db 810 CCAGTGGCCATTCATGACGAGCGGATCATGTGTTTACACATGAAGATCAAGAGTCAGGC 869

QY 1279 CGTGGTGTTCCTGAGGAGCCAGAAATCAGCGAGGAGCTCAAGGACCTGATCTCTGAAGAT 1338

```
Db      870  CCTGGAATTTCCAGACCAGCCGACATAGCTGAGGACTTGAAGGACCTGATCACCCGTTAT 929
Qy      1339 GTTAGACAGATCCGAGACGAGATTCGGGTGCGAGACATCAAGTTGCACCTTGGGT 1398
Db      930  GCTGGACAAGAACCCGAGTCGAGGATCGGTGCGGGAATCAAGCTGCACCCCTGGGT 989
Qy      1399 GACCAAGAACCGGAGAGCCCTTCTCTCGAGGAGGACACTGCAGCGTGTGGAGGT 1458
Db      990  CACGAGCATGGGCGGAGCGGTTCGCTCGGAGGATGAGAACTGCACGCTGCTCGAAGT 1049
Qy      1459 GACAGAGGGGAGGTTAAGAACTCAGTCAGGCTCATCCCGAGCTGAGACACAGGTGATCCT 1518
Db      1050 GACTGAAGAGGAGGTCGAGAACTCAGTCAAAACATTTCCAGCTTGGCAACCGTGATCCT 1109
Qy      1519 GGTGAAGTCCATCTGAGGAGGTTCTTCTGGGAAACCGGTTTGGGACCCCGTTCAGCCGAG 1578
Db      1110 GGTGAAGACCATGATACGTAACGCTCTTGGGAACCCATTCGAGGC---AGCCGGCG 1166
Qy      1579 GGAAGAGCGATCCATGCTGCTCCAGGAAACCTACTGTTGAAAGAGGGTTTGGTGAAGG 1638
Db      1167 GGAGGAACGCTCACTGTCAGCGCTGGAACCTTCTCACCAAAACCAACCAAGGAATG 1226
Qy      1639 GGGCAAGAGCCCGAGCTC 1657
Db      1227 TGAGTCCCTGCTCGAGCTC 1245
```

RESULT 14

ADB75229

ID ADB75229 standard; cdna; 1804 BP.

AC ADB75229;

DT 04-DEC-2003 (first entry)

DE Prostate cancer marker cdna.

XX Prostate; cancer; cytostatic; gene therapy; marker; ss.

XX Homo sapiens.

XX WO2003009814-A2.

XX 06-FEB-2003.

XX 25-JUL-2002; 2002WO-US023913.

XX 25-JUL-2001; 2001US-0307982P.

XX 22-AUG-2001; 2001US-0314356P.

XX 25-SEP-2001; 2001US-0325020P.

XX 12-DEC-2001; 2001US-0341746P.

XX 03-MAR-2002; 2002US-0362158P.

XX (MILL-) MILLENNIUM PHARM INC.

XX Schlegel R, Monahan JE, Endege WO, Gannavarapu M, Gorbacheva B;

XX Hoersh S, Kamatkar S, Wonsey AM, Glatt K, Zhao X, Anderson D;

XX WPI; 2003-248033/24.

XX New nucleic acid molecule, useful for diagnosing or treating prostate

XX cancer.

XX Disclosure; SEQ ID NO 53; 99pp; English.

XX The invention relates to newly discovered cancer markers associated with

XX the cancerous state of prostate cells. Also disclosed is a method of

XX assessing whether a patient is afflicted with prostate cancer. The method

XX of the invention involves assessing whether a patient is afflicted with

XX prostate cancer by comparing the level of expression of a marker in a

XX patient sample and the normal level of expression of the marker in a

XX control non-prostate cancer sample, where a significant increase in the

CC level of expression of the marker in the patient sample and the normal
CC level indicates that the patient is afflicted with prostate cancer.
CC Nucleic acids of the invention are useful for diagnosing or treating
CC prostate cancer, and may be useful in gene therapy. Sequences given in
CC ADB75177-ADB75631 represent marker cDNA and proteins. Note: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

XX
SQ Sequence 1804 BP; 445 A; 519 C; 453 G; 387 T; 0 U; 0 Other;

Query Match 29.7%; Score 651; DB 9; Length 1804;

Best Local Similarity 71.5%; Pred. No. 1.5e-131;

Matches 871; Conservative 0; Mismatches 345; Indels 3; Gaps 1;

```
Qy      439  GCCTTATGCCACGGGCGCTGCCAGCCACATCTCCCCCGGGCTGGCGGAGGCCACCAT 498
Db      30  GCCTTACTACCGCTCAGCTCCCGCAGTCTCTGCTCGGCTGCCCGGGCGCGACGT 89
Qy      499  CGAGTCCCACACGTCGCCATCTCAGATGCAGAGGACTGCTGTCAGTGAACACGATACAA 558
Db      90  GGAAGTCTCACACGCTCTCCATCACGGGTATGCAGGACTGTGTGCACTGAATCAGTATAC 149
Qy      559  GCTGCAGAGTGAGATTGGCAAGGTGCTTACGCTGTGTGCTGAGCTGGCTCAACACCAAG 618
Db      150  CTTGAAGGATGAAATTTGAAAGGGCTCTATGCTGTCGTCAGTTGGCTTACAAAGAAA 209
Qy      619  TGAAGACGACACTATGCAATGAAAGTCTCTTCCAAAAAGAGTTACTGAAGCAGATATGG 678
Db      210  TGACATATCTACTATGCAATGAAAGTGTCTGTCCAAAAGAGAGCTGATCCGGCAGGCCG 269
Qy      679  CTTTCCACGTCGCCCTCCCCCGAGAGGGTCCAGGTGCCCCAGGGAGGACACGCCAAGCA 738
Db      270  CTTTCCAGCTCGCCCTCCACCCGAGGACACCGGCCAGCTCTCTGAGGCTGCATCCAGCC 329
Qy      739  GCTGCTGCCCTCGAGGGGTGTACAGGAGATTGCCATCTCTCAAGAGCTTGACACCACT 798
Db      330  CAGGGGCCCATTTGAGCAGGTGTACAGGAAATTTGCCATCTCTCAAGAGCTTGACACCA 389
Qy      799  GAATGTGTCAAACTGATCGAGCTCTGATGATGATGATGATGATGATGATGATGATGAT 858
Db      390  CAATGTGTCAGCTGTGTGAGGTCTGTGATGATGATGATGATGATGATGATGATGATGAT 449
Qy      859  GTTTGACCTCTCAGAAAGGGGCCGTCATGGAAGTGCCTGTGACAAAGCCCTTCTCGGA 918
Db      450  GTTTCGAATGCTGTCAAACCAAGGGGCCGTCATGGAAGTGCCTGATGATGATGATGATGAT 509
Qy      919  GGAGCAAGCTCGCCTTACCTCGGGAGCTCATCTCGGGCTCGAGTCTGACACTGCCA 978
Db      510  AGACCAAGGGCCGTTTCTACTTCCAGGATCTGATCAAAAGGCTCGAGTCTTACACTACCA 569
Qy      979  GAAGATCGTCCACAGGAGACATCAAGCCATCAACCTCTCTCTGGGGGATGATGGCACGT 1038
Db      570  GAAGATCATCCACCGTGACATCAACCTTCCACCTCTCTGTCGAGAGAGATGGGCACAT 629
Qy      1039 GAAGATCGCGACTTTTGGCTCAGCAACACGTTTGAAGGAAACGACGCTCAGCTGTCCAG 1098
Db      630  CAAGATCGCTGACTTTTGGTGTGAGCAATGAATTCAGGGCAGTGAACGCGCTCTCTCCAA 689
Qy      1099 CACGGCGGAAACCCAGACATTCATGGCCCCCGAGGCACTTCTGATTTCCGGCCAGAGCTT 1158
Db      690  CACCGTGGCACCGCCGCTTCTATGGCACCCCGAGTGTCTCTCTGAGACCCCGAAGATCTT 749
Qy      1159 CAGTGGGAAGGCTTGGATGTATGGGCCACTGGCGTCACTGTCTGTCTGTCTGTCTATGG 1218
Db      750  CTCTGGGAAGGCTTGGATGTATGGGCCATGGGTGTGACACTATACTGCTTGTCTTTGG 809
Qy      1219 GAAGTGCCTTATCATGACGATTTCTATCTCGGCCCTCCACAGGAAGATCAAGATGAGCC 1278
Db      810  CCAGTGCCTTATCATGACGAGCGGATCATGTGTTTACACAGTAAGATCAAGAGTCAGGC 869
Qy      1279 CGTGGTGTCTCTGAGAGGACCAAAATCACGGGAGCTCAAGGACCTGATCTCTGAAGAT 1338
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QY 1159 CAGTGGGAAGGCCTTTGGATGTATATGGGCCACTGGCGCTACGTTGTACTGCTTTGTCTATGG 1218
Db |||||
1226 CTCTGGGAAGGCCTTTGGATGTATATGGGCCACTGGCGCTACGTTGTACTGCTTTGTCTATGG 1285
QY 1219 GAAGTGCCCATTCATCGAGGATTTTCATCTGCGCCCTCCACAGGAGAGATCAAGATGAGCC 1278
Db |||||
1286 CCAGTGCCCATTCATCGAGGATTTTCATCTGCGCCCTCCACAGGAGAGATCAAGATGAGCC 1345
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Job time : 1246 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 11, 2004, 17:48:37 ; Search time 13554 Seconds
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Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a

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and is derived by analysis of the total score distribution.

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DEFINITION Sequence 1 from patent US 6426206.
ACCESSION AR221281
VERSION AR221281.1 GI:23328248
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2190)
AUTHORS Wei, M.-H., Di Francesco, V. and Beasley, E.M.
TITLE Isolated human kinase proteins, nucleic acid molecules encoding human kinase proteins, and uses thereof
JOURNAL Patent: US 6426206-A 1 30-JUL-2002;

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DEFINITION Sequence 1 from Patent WO0224920.
ACCESSION AX406674
VERSION AX406674.1 GI:21439624
KEYWORDS
SOURCE
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Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Beasley,E.M., Wei,M.H., Bonazzi,V.R., Sanders,R.C. and di
Francesco,V.C.
TITLE Isolated human kinase proteins, nucleic acid molecules encoding
human kinase proteins, and uses thereof
JOURNAL Patent: WO 0224920-A 1 28-MAR-2002;
PE Corporation (NY) (US)
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QY	1681	TGCATCTGAGCCCTGATGCACGAGGGCACCCGGCAGACACTCATCTCCGGGCTC	1740
Db	1681		
QY	1741	CAGAGGCCACCTCATGCAACAGCCGCCCGCAGGACGAGCTGGGACTTCGAGCC	1800
Db	1741		
QY	1801	CCACTCCCGCCCTCCCTCATGCTGTCATGACCTCCAGCAGCGCTCCAGGGACAG	1860
Db	1801		
QY	1861	ACTGGATGATGTCATTTGGGCTTGGGGGCGAGGCTCCAGAGGCCATCTCTCTCT	1920
Db	1861		
QY	1921	TCTTGGCCCTCTTGGCCCTGACCCATCTGTGGGGAACCGGCTGCCCATGGAGCTCAG	1980
Db	1921		
QY	1981	AAATGCCACCCGGCTGGTTGGCTGATGCTGGGGCAGGAGGAGGAGGAGCAAGAT	2040
Db	1981		
QY	2041	GGCAGGTGGAGCGCAGGCTTACCACACGAGAGAGCTCCCGCTGGGCGGCGAGGCC	2100
Db	2041		
QY	2101	TGGCTCAGCTCCACAGCATATGTTGAGAGGGGGGTACCTGCCACCTTGGGGTGGT	2160
Db	2101		
QY	2161	GGCACAGAGCTTTGTTCTATTCAGAGCT	2190
Db	2161		
RESULT 3			
LOCUS	HSMB01550	3583 bp	linear
DEFINITION	Homo sapiens mRNA; cDNA DKFZp761M0423 (from clone DKFZp761M0423); complete cds.		
ACCESSION	AL136576		
VERSION	AL136576.1	GI:13276654	
KEYWORDS	Homo sapiens (human)		
SOURCE	Homo sapiens		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE	1		
AUTHORS	Wiemann, S., Weil, B., Wellenreuther, R., Gassenhuber, J., Glassl, S., Ansorge, W., Boecker, M., Bloeker, H., Bauersachs, S., Blum, H., Lauber, J., Duesterhoeft, A., Beyer, A., Koehler, K., Strack, N., Mewes, H. W., Ottenwaelder, B., Obermaier, B., Tampe, J., Heubner, D., Wambutt, R., Korn, B., Klein, M. and Poustka, A.		
TITLE	Toward a catalog of human genes and proteins: sequencing and analysis of 500 novel complete protein coding human cDNAs		
JOURNAL	Genome Res. 11 (3), 422-435 (2001)		
MEDLINE	21154917		
PUBMED	11230166		
REFERENCE	2 (bases 1 to 3583)		
AUTHORS	Bloeker, H., Boecker, M., Brandt, P., Mewes, H. W., Weil, B. and Wiemann, S.		
TITLE	Direct Submission		
JOURNAL	Submitted (18-JAN-2000) MIPS, Am Klopferspitze 18a, D-82152		
COMMENT	Martinsried, GERMANY Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; sequenced by GBF (National Research Centre for Biotechnology Ltd., Braunschweig/Germany) within the cDNA sequencing consortium of the German Genome Project. This clone is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzd.de Further information about the clone and the sequencing project is available at http://www.mips.biochem.mpg.de/proj/cDNA/.		
FEATURES	Location/Qualifiers 1..3583 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="RZPD:DKFZp761M0423" /map="26.0 cR from top of Chr17 linkage group" /clone="DKFZp761M0423" /tissue_type="amygdala" /clone_lib="761 (synonym: hamy2). Vector pSport1; host DH10B; sites NotI + SalI" /dev_stage="adult" 1..3583 /gene="DKFZp761M0423" 149..1666 /gene="DKFZp761M0423" /note="similarity to Cam-kinase alpha (Rattus norvegicus)" /codon_start=1 /product="hypothetical protein" /protein_id="CAB66511.1" /db_xref="GI:13276655" /db_xref="GOA:Q9BQH3" /translat="MEGPAVCCQDPRAELVRAADIVTHLEADGGPEPRNGVDP PPARAASVPIGSTRLLPARPSLSARKLSLOERPAGSYLEAOAGPYATGPASHISPR AWRPTTESHHVAISDAEDCVOLNOYKLOSEIGKAGVGVRLAVNESEDRHVAMKVL KKLLKQYGFPRPPRPGSQAAQGGPAKQLPLERVQBIALIKLKHVNKKVILVLD DDPAEDNLVYLDLLRKGPMVEVPCDFSEEQARLYLRDVLGLLEYLHCOQIVRHED KPNLLLGDDHVKIADPVSQNPEDNAQISSSTAGTAPFAPEAIDSQGSFGKAL DVWATGVLYCFVYKCPFIIDDFILALHRIKNEPVVFPPEPEISEELKDIILKMLDK NPETRIGVDPIDKLHPWVTNKEBPLPSEEBHCSVVEVEEVKNSVLITPSWTVILV KSMLRKESFGNPFEPQARREERSMSAPGNLLVKEGFGGKSPGLPQVEDEAS"		
polyA_signal	3525..3530 /gene="DKFZp761M0423"		
polyA_site	3546 /gene="DKFZp761M0423"		
ORIGIN	Query Match 98.7%; Score 2161.2; DB 9; Length 3583; Best Local Similarity 99.9%; Pred. No. 0; Matches 2163; Conservative 0; Mismatches 3; Indels 0; Gaps 0;		
QY	25	CTGGGCCCCCAGCAGCGCGTGGGCGCGGGCGGGCGGGCGGGCGGGCGGAGGCGA	84
Db	1	CTGGGCCCCCAGCAGCGCGTGGGCGCGGGCGGGCGGGCGGGCGGGCGGAGGCGA	60
QY	85	GTGGGCGCGCGCGCGCGCGCGACACTGTGCGCGCGCGCGCGCGCGCGCGCGCT	144
Db	61	GTGGGCGCGCGCGCGCGCGCGACACTGTGCGCGCGCGCGCGCGCGCGCGCT	120
QY	145	ACGCAGAGAAGAACCCCTTGTGACTGAAGCAATGGAGGGGGGTCAGCTCTCTGCT	204
Db	121	ACGCAGAGAAGAACCCCTTGTGACTGAAGCAATGGAGGGGGGTCAGCTCTCTGCT	180
QY	205	TCCTCGGGCAGAGCTGGTAGAACGGGTGGGAGCCATCGATGTGACTCACTTGGAG	264
Db	181	TCCTCGGGCAGAGCTGGTAGAACGGGTGGGAGCCATCGATGTGACTCACTTGGAG	240
QY	265	AGATGGTGGCGCCAGAGCTTACTAGAACGGGTGGGAGCCCGCCCGCCAGAGCTGC	324
Db	241	AGATGGTGGCGCCAGAGCTTACTAGAACGGGTGGGAGCCCGCCCGCCAGAGCTGC	300

325 QY CTCTGTGATTCCTGGCAGTACTTCAAGACTGCTCCAGCCGCGCTTAGCCTCTCAAGCCAG 384
Db CTCTGTGATTCCTGGCAGTACTTCAAGACTGCTCCAGCCGCGCTTAGCCTCTCAAGCCAG 360
385 QY GAAGCTTTCCCTACAGGAGGGCCAGCAGGAGCTATCTGGAGGCCAGGCTGGGCTTTA 444
Db GAAGCTTTCCCTACAGGAGGGCCAGCAGGAGCTATCTGGAGGGCCAGGCTGGGCTTTA 420
445 QY TCCCAACGCGGCTGCGCAGCAATCTCCCGCGGGCTGCGGAGGCCACCAATCAAGTC 504
Db TGCACAGGGGCTGCGCAGCAATCTCCCGCGGGCTGCGGAGGCCACCAATCAAGTC 480
505 QY CCACCACTGGGCCATCTCAGATGCAAGAGACTGCGTGCAAGTGAACAGTCAAGCTGCA 564
Db CCACCACTGGGCCATCTCAGATGCAAGAGACTGCGTGCAAGTGAACAGTCAAGCTGCA 540
565 QY GAGTGAGATTGCAAGGCTGCTACGAGTGTGGTGAGGCTGGCTACAAAGAAAGTGAAG 524
Db GAGTGAGATTGCAAGGCTGCTACGAGTGTGGTGAGGCTGGCTACAAAGAAAGTGAAG 600
625 QY CAGACACTATGCAATGAAAGTCTTTCCAAAGAAAGTTACTGAAGCAGTATGGCTTTCC 684
Db CAGACACTATGCAATGAAAGTCTTTCCAAAGAAAGTTACTGAAGCAGTATGGCTTTCC 660
685 QY AGTGCGCTTCCCGCAGAGGGTCCAGAGTGCAGGGAGGACCAAGCAAGCAGCTGCT 744
Db AGTGCGCTTCCCGCAGAGGGTCCAGAGTGCAGGGAGGACCAAGCAAGCAGCTGCT 720
745 QY GCCCTGGAGCGGTGTACAGAGATTGCCATCTCTGAAGAGCTGGACCAAGTGAATCT 804
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805 QY GGTCAAACTGATCGAGGCTCTGATGACCCAGCTGAGGACCAACTCTATTGTGTTTGA 864
Db GGTCAAACTGATCGAGGCTCTGATGACCCAGCTGAGGACCAACTCTATTGTGTTTGA 840
865 QY CTCTCTGAGAAAGGGGCCGCTCATGAAAGTGCCCTGTGCAAGCCCTTCTGGAGAGCA 924
Db CTCTCTGAGAAAGGGGCCGCTCATGAAAGTGCCCTGTGCAAGCCCTTCTGGAGAGCA 900
925 QY AGCTCGCTCTACCTGGGAGCGTCACTCTGGGCTCGAGTACTTCGACTGCCAGAGAT 984
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985 QY CGTCCAAGGGAATCAAGGCATCCAACTGCTCTGGGGATGATGGGCACTGGAAGAT 1044
Db CGTCCAAGGGAATCAAGGCATCCAACTGCTCTGGGGATGATGGGCACTGGAAGAT 1020
1045 QY CGCGCATTTGGGCTCAGCAACAGTTTGAAGGGGAACGACGCTCAGCTGTCAGCAAGCGC 1104
Db CGCGCATTTGGGCTCAGCAACAGTTTGAAGGGGAACGACGCTCAGCTGTCAGCAAGCGC 1080
1105 QY GGGAAACCCAGCATTATGSCCCCCGAGGCCATTTCTGATTCGGGCCAGAGCTTCAGTGG 1164
Db GGGAAACCCAGCATTATGSCCCCCGAGGCCATTTCTGATTCGGGCCAGAGCTTCAGTGG 1140
1165 QY GAAGGCTTTGGATGATGGGCCACTGGCGTCACTGCTTGTACTGCTTGTATGGGAAGTG 1224
Db GAAGGCTTTGGATGATGGGCCACTGGCGTCACTGCTTGTACTGCTTGTATGGGAAGTG 1200
1225 QY CCATTTATCGACGATTTATCTCGCCCTCCACAGGAAGATCAAGAAATGAGCCGTGGT 1284
Db CCATTTATCGACGATTTATCTCGCCCTCCACAGGAAGATCAAGAAATGAGCCGTGGT 1260
1285 QY GTTTCCTGAGGAGCGAAGATCAGCGAGGCTCAAGGACCTCATCTGAGAGTGTAGA 1344
Db GTTTCCTGAGGAGCGAAGATCAGCGAGGCTCAAGGACCTCATCTGAGAGTGTAGA 1320
1345 QY CAAGAATCCCGACGAGAAATTTGGGGTCCAGACATCAAGTTGCACCTTTGGGTGACCAA 1404
Db CAAGAATCCCGACGAGAAATTTGGGGTCCAGACATCAAGTTGCACCTTTGGGTGACCAA 1380

1405 QY GAAACGGGAGGAGCCCTTCCTTCGAGGAGAGACACTGACGGTGGTGGAGGTGACAGA 1464
Db GAAACGGGAGGAGCCCTTCCTTCGAGGAGAGACACTGACGGTGGTGGAGGTGACAGA 1440
1465 QY GGGGAGGTTAAGAACTCAGTCAGGCTCATCCAGCTGGAACACCGTGTATCTCTGTGAA 1524
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1585 QY GCGATCCATGCTGCTCAGGAAACCTACTGGTGAAGAGGGTTTGGTGAAGGGGGCAA 1644
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1645 QY GAGCCACAGAGCTCCCGCGGCTCCAGGAGACAGAGGCTGATCTGAGCCCTTGCATGCAC 1704
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1705 QY CCAGGCCCACCCGGCAGCACACTCATCCCGCGCTCCAGAGGCCACCCCTCATGCAACA 1764
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1885 QY CTTGGGGCAGGGCTCCACAGAGGCATCTCTCTTTTGGCCCTCTTGGCCTGACCC 1944
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2005 QY GCCTTGGGCGCAGGAGCAGGAGCAGGAGACCAAGATGGCAGTGGAGGCGAGGCTTACCA 2064
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2065 QY CAAACGGAAGAGACCTCCCGCTGGGGCCGGCCTGAGCTCAGCTGCAAGGCAATATG 2124
Db CAAACGGAAGAGACCTCCCGCTGGGGCCGGCCTGAGCTCAGCTGCAAGGCAATATG 2100
2125 QY GTGGAGAGGGGGTACCTTCCACCTTGGGGTGGTGGCACCAGAGCTCTTGTCTATTCA 2184
Db GTGGAGAGGGGGTACCTTCCACCTTGGGGTGGTGGCACCAGAGCTCTTGTCTATTCA 2160
2185 QY GACGCT 2190
Db GACGCT 2166

RESULT 4

BC043487

LOCUS

DEFINITION

Homo sapiens

alpha, transcript variant 1, mRNA (cDNA clone MGC:49844

IMAGE:571570), complete cds.

ACCESSION

BC043487

VERSION

BC043487.1

KEYWORDS

Homo sapiens (human)

SOURCE

Homo sapiens

ORGANISM

REFERENCE

AUTHORS

BC043487 3575 bp mRNA linear PRI 07-OCT-2003
Homo sapiens calcium/calmodulin-dependent protein kinase 1,
alpha, transcript variant 1, mRNA (cDNA clone MGC:49844
IMAGE:571570), complete cds.

BC043487
BC043487.1 GI:27694083

MGC.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 3575)

Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,

Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.W., Schuler,G.D.,


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QY 949 CATCTTGGSCCTCGAGTACTTGCACATGCCAGAGATCGTCCACAGGACATCAAGCCATC 1008
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QY 1129 CGAGGCCATTTCTGATTCGGCCAGAGCTTCAGTGGGAAGGCTTGGATGTATGGCCAC 1188
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Db 1801 GTCCAGGACAGACTGGAATGATGTCATTTGGGGTCTTGGGGGAGGAGGCTCCACGAG 1860
QY 1909 CCATCTCTCTTCTTGGCCCTCTTGGCCCTGACCCCATCTGCTGGGGAAACCGGGTGCCC 1968
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QY 2029 GGAGACCAAGATGGCAGGTGGAGGCCAGCTTACCACACGGAAGAGACTCCCGCTGG 2088
Db 1981 GGAGACCAAGATGGCAGGTGGAGGCCAGCTTACCACACGGAAGAGACTCCCGCTGG 2040
QY 2089 GCCGGGCGAGGCTGGCTCAGCTGCCACAGGATATGGTGGAGAGGGGGGTACCTCGCCCA 2148
Db 2041 GCCGGGCGAGGCTGGCTCAGCTGCCACAGGATATGGTGGAGAGGGGGGTACCTCGCCCA 2100
QY 2149 CTTGGGGTGGTGGCACCAGAGCTCTTGTCTATTAGAGCT 2190
Db 2101 CTTGGGGTGGTGGCACCAGAGCTCTTGTCTATTAGAGCT 2142

RESULT 5
AF425232
LOCUS
DEFINITION Homo sapiens CamKK alpha protein mRNA, complete cds.
ACCESSION AF425232
VERSION AF425232.1 GI:23499313
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 3536)
AUTHORS Tascadda,F., Carra,S., Harvey,M. and Barden,N.
TITLE Characterization of human CamKK alpha gene structure
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 3536)
AUTHORS Tascadda,F., Carra,S., Harvey,M. and Barden,N.
TITLE Direct Submission
JOURNAL Submitted (27-SEP-2001) Pharmacology, University of Modena and
Reggio Emilia, Campi 183, Modena, MO 41100, Italy
FEATURES
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CDS
Query Match 96.5%; Score 2114.2; DB 9; Length 3536;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2116; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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ORIGIN

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Db 1 GCAGCAGGAGCAGTGGGGCCCGCCCGCGGCGCACACGACACTGTCCCGCGGCCAGGT 60
QY 132 TCCCAACAGGCTACGACAGAGAACCCCTTGTACATGAAGCATGGAGGGGGTCCAGCTG 191
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Qy 252 ACTTGGAGGAGCAGATGGTGGCCAGAGCCTACTAGAAACGGTGTGGACCCGCCACAC 311
Db 181 ACTTGGAGGAGCAGATGGTGGCCAGAGCCTACTAGAAACGGTGTGGACCCGCCACAC 240
Qy 312 GGGCCAGAGCTGCTGTGTGATCCTGTGCAGTACTTCAAGACTCTCCAGCCCGGCGCTA 371
Db 241 GGGCCAGAGCTGCTGTGTGATCCTGTGCAGTACTTCAAGACTCTCCAGCCCGGCGCTA 300
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Db 661 CCAAGCAGCTGCTGCCCTGAGCGGGTGTACAGGAGATTGCCATCCTGAAAGAGCTGG 720
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Qy 912 TCTCGGAGGAGCAAGCTCGCCTTACCTCGGGAGCTCATCTGGGCTCGAGTACTTGC 971
Db 841 TCTCGGAGGAGCAAGCTCGCCTTACCTCGGGAGCTCATCTGGGCTCGAGTACTTGC 900
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DEFINITION
AF425301
ACCESSION
AF425301.1 GI:23499315
VERSION
KEYWORDS
Homo sapiens (human)

ORGANISM	Homo sapiens	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
AUTHORS	1 (bases 1 to 3529)	
TITLE	Harvey, M., Carra, S., Tascetta, F. and Barden, N.	
JOURNAL	Characterization of human CAMKK alpha gene structure	
Unpublished		
REFERENCE	2 (bases 1 to 3529)	
AUTHORS	Harvey, M., Carra, S., Tascetta, F. and Barden, N.	
Direct Submission		
JOURNAL	Submitted (27-SEP-2001) Neuroscience, CHUL, 2705 Blvd. Laurier, Ste-Foy, Quebec G1V4G2, Canada	
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LOCUS Sequence 14 from Patent WO0146397.
DEFINITION AX179641
ACCESSION AX179641
VERSION AX179641.1 GI:15132054
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE 1
AUTHORS Yang, J., Baughn, M.R., Burford, N., Au-Young, J., Lu, D.A., Reddy, R.,
Yue, H., Yao, M.G., Lal, P. and Khan, F.A.
TITLE Human kinases
JOURNAL Patent: WO 0146397-A 14 28-JUN-2001;
Incyte Genomics, Inc. (US)
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DEFINITION Sequence 39 from Patent WO0208399.
ACCESSION AX746188
VERSION AX746188.1 GI:31746174
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE
AUTHORS

1 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Yue, H., Khan, F.A., Gururajan, R., Hafalia, A.J., Chawla, N.K.,
Arvizu, C.S., Ramkumar, J., Gandhi, A.R., Policky, J.L., Baughn, M.R.,
Tribouley C.M., Bandman, O., Nguyen, D.B., Lu, Y., Burford, N., Lal, P.,
Ding, L., Yao, M.G., Elliott, V.S., Recipon, S.A., Kearney, L., Lu, D.A.,
Greenwald, S.R., Tang, Y.T., Wang, Y.F., Walsh, R.T., Gietzen, K.J.,
Yang, J., Jackson, J.L. and Thornton, M.
Human kinases

TITLE
JOURNAL

Patent: WO 0208399-A 39 31-JAN-2002;
Incyte Genomics, Inc. (US) ; Thornton, Michael (US)

FEATURES
source

Location/Qualifiers
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Matches 1910; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
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862	DB	GCATGCCAGAAGATCGTTCACAGGAGCATCAAGCGATCCAACTGTCTCTGGGGGATGA	921
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1450	QY	GGTGAGGTGACAGAGGGGGAGGTTAAGAACTCAGTCAGGCTCATCCCCAGCTCGACAC	1509
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QY 1990 CCGCTGGTTGGTCATGTCCTGGGCGCAGGAGCAGAGCGACGACGACCAAGATGGCAG 2045
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RESULT 9
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 ACCESSION AX455761
 KEYWORDS AX455761.1 GI:21714788
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 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
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 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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 REFERENCE
 AUTHORS Meyers, R.A. and Silos-Santiago, I.
 TITLE 16658, 14223, and 16002, novel human kinases and uses therefor
 JOURNAL Patent: WO 0220800-A 7 14-MAR-2002;
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 Best Local Similarity 98.9%; Pred. No. 1.1e-312;
 Matches 1652; Conservative 4; Mismatches 13; Indels 1; Gaps 1;

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DB 693 AAGCAGTATGGCTTTCCACGTCGCCCTCCCGCAGAGGGTCCAGGCTGCCAGGGAGGA 752
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DB 933 CCTTCTCCGAGGAGCAGCTGCTGCTCTACCTGCGGGAAGTATCTCTGGGCTCGAGTAC 992
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RESULT 10
AX455763
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
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AX455763
AX455763.1 GI:21714790
Homo sapiens (human)
Homo sapiens
Mammalia; Euthera; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE
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AUTHORS
TITLE
JOURNAL
FEATURES
Source

Meyers R.A. and Silos-Santiago I.
16658, 14223, and 16002, novel human kinases and uses therefor
Patent: WO 0220800-A 9 14-MAR-2002;
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ORIGIN

Query Match 68.1%; Score 1490.6; DB 6; Length 1683;
Best Local Similarity 99.4%; Pred. No. 5.9e-284;
Matches 1496; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

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VERSION AX166519.1 GI:14546864
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Plowman,G.D., Whyte,D., Manning,G.S., Sudarsanam,S.S., Martinez,R.,
Flanagan,P. and Clary,D.S.
TITLE Novel human protein kinases and protein kinase-like enzymes
JOURNAL Patent: WO 0138503-A 10 31-MAY-2001;
Sugen, Inc. (US)
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DEFINITION	Homo sapiens calcium/calmodulin-dependent protein kinase 1, alpha, transcript variant 3, mRNA (cDNA clone MGC:34095 IMAGE:5175128), complete cds.		
ACCESSION	BC031647		
VERSION	BC031647.1	GI:21594835	
KEYWORDS	MGC.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		

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Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shennan, C.M., Schuler, G.D., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, K., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stalton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Udine, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Lequellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.C., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smal, D.E., Scherch, A., Schein, J.E., Jones, S.J., and Marra, M.A.	
Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences	
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)	
22388257	
2 (bases 1 to 2469)	
Strausberg, R.	
Direct Submission	
Submitted (06-JUN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA	
NIH-MGC Project URL: http://mgc.nci.nih.gov	
Contact: MGC help desk	
Email: cgabs-r@mail.nih.gov	
Tissue Procurement: Life Technologies, Inc.	
cDNA Library Preparation: Life Technologies, Inc.	
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)	
DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center	
Center code: BCM-HGSC	
Web site: http://www.hgsc.bcm.tmc.edu/cdna/	
Contact: amg@bcm.tmc.edu	
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseg, H., Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati, A.N., Gibbs, R.A.	
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov	
Series: IRAK plate: 51 Row: 1 Column: 23	
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Qy 151 AAGAACCCCTTGACTAGCAATGGAGGGGGTCCAGCTGTCTGCTGCCAGGATCCTCG 210
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Qy 211 GGCAGAGCTGTAGAAACGGGTGGCAGCCATCGATGTGACTCACCTTGAGGAGGCGAGATGG 270
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Qy 451 GGGGCGCTGCCAGCACATCTCCCGCGGCGCTGGGAGGAGGCCACCATCGAGTCCCACCA 510
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ACCESSION BC017529
VERSION BC017529.1
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SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Mammalia; Eutheria; Rodentia; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Muridae; Murinae; Mus.
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AUTHORS	Krausberg,R.I., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altshul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Schecterson,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullaby,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Fulyk,S.W., Villalón,D.K., Muzny,D.M., Sodergren,E.J., Iu,X., Gibbs,R.A., Fahy,J., Helton,E., Kettelman,M., Madan,A., Rodrigues,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smalish,D.E., Schnerker,A., Schein,J.E., Jones,S.J., and Marra,M.A.	
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences	
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)	
MEDLINE	22388257	
PUBMED	12477932	
REFERENCE	2 (bases 1 to 3435)	
AUTHORS	Strausberg,R.	
TITLE	Direct Submission	
JOURNAL	Submitted (19-NOV-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA	
REMARK	NIH-MGC Project URL: http://mgc.nci.nih.gov	
COMMENT	Contact: MGC help desk Email: cgabbs@mail.nih.gov Tissue procurement: Jeffrey E. Green, M.D. CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Genome Sequence Centre, BC Cancer Agency, Vancouver, BC, Canada info@bcqsc.bc.ca Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Leticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Nesse, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline Schein, Duane Smalish, Michael Smith, Lorraine Spence, Jeff Scott, Michael Thorne, Miranada Teai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.	
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AUTHORS		J. Biochem. 119 (6), 1176-1181 (1996)	
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MEDLINE		Fujisawa, H. and Okuno, S.	
PUBMED		8827455	
REFERENCE		Submitted (15-FEB-1999) Hitoshi Fujisawa, Asahikawa Medical	
AUTHORS		College, Department of Biochemistry; Nishikagura 4-5-3-11,	
TITLE		Asahikawa 078-8510, Japan [E-mail: okuno@asahikawa-med.ac.jp,	
JOURNAL		Tel:+81-166-68-2340, Fax:+81-166-68-2349)	
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

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Total number of hits satisfying chosen parameters: 1017041

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Listing first 45 summaries

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- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_virus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2626	99.7	505	4 Q8BQH3	Q8bqh3 homo sapien
2	2470	93.8	520	4 Q8NS59	Q8ns59 homo sapien
3	2468	93.7	505	11 P97756	P97756 rattus norv
4	2461	93.4	505	11 Q8VB22	Q8vby2 mus musculu
5	2452	93.1	505	11 Q84572	Q84572 rattus norv
6	2419	91.8	505	11 Q9R054	Q9r054 mus musculu
7	1834	69.6	523	13 Q8AYR1	Q8ayr1 xenopus lae
8	1537.5	58.4	541	4 Q8WV04	Q8wy04 homo sapien
9	1536	58.3	541	4 Q81UG3	Q81ug3 homo sapien
10	1525.5	57.9	557	4 Q94883	Q94883 homo sapien
11	1525	57.9	541	11 Q9QZT7	Q8qzt7 mus musculu
12	1518.5	57.6	533	4 Q96RR3	Q96rr3 homo sapien
13	1518.5	57.6	588	4 Q96RR4	Q96rr4 homo sapien
14	1517	57.6	533	4 Q96RP2	Q96rp2 homo sapien
15	1517	57.6	588	4 Q96RP1	Q96rp1 homo sapien
16	1498	56.9	588	4 Q9Y5N2	Q9y5n2 homo sapien

17	1495	56.8	588	11 Q8C078	Q8c078 mus musculu
18	1494	56.7	587	11 Q88831	Q88831 rattus norv
19	1488	56.5	588	11 Q8CH42	Q8ch42 mus musculu
20	1472.5	55.9	417	4 Q9UER3	Q9uer3 homo sapien
21	1422	54.0	579	11 Q8C0G3	Q8c0g3 mus musculu
22	1358.5	51.6	503	11 Q8BXN8	Q8bxn8 mus musculu
23	1342	50.9	498	4 Q8WY03	Q8wy03 homo sapien
24	1340.5	50.9	498	4 Q8IUG2	Q8iug2 homo sapien
25	1323	50.2	545	4 Q8WY05	Q8wy05 homo sapien
26	1321.5	50.2	490	4 Q8WY06	Q8wy06 homo sapien
27	1197.5	45.5	419	11 Q80TS0	Q80ts0 mus musculu
28	1047	39.7	432	5 Q8T8D4	Q8t8d4 caenorhabdi
29	1037	39.4	365	4 Q8N314	Q8ni14 homo sapien
30	949	36.0	269	4 Q9BWE9	Q9bwe9 homo sapien
31	629.5	23.9	180	4 Q9UES2	Q9ues2 homo sapien
32	557	21.1	518	3 Q9Y898	Q9y898 emericella
33	527.5	20.0	420	10 Q9AUR9	Q9aur9 oryza sativ
34	526.5	20.0	396	10 Q93V58	Q93v58 arabidopsis
35	520.5	19.8	407	10 Q8LP06	Q8lp06 arabidopsis
36	512	19.4	382	10 Q9M175	Q9m175 arabidopsis
37	503	19.1	402	10 Q9FKJ2	Q9fkj2 arabidopsis
38	478.5	18.2	217	3 Q9UTZ4	Q9utz4 schizosacch
39	468	17.8	1246	3 Q9P3E9	Q9p3e9 neurospora
40	448	17.0	440	10 Q24343	Q24343 sorghum bic
41	446.5	17.0	452	10 Q84V03	Q84vq3 arabidopsis
42	437	16.6	440	10 Q24342	Q24342 sorghum bic
43	436.5	16.6	511	10 Q40544	Q40544 nicotiana t
44	434	16.5	461	10 Q82051	Q82051 sorghum bic
45	431.5	16.4	514	10 Q9M726	Q9m726 lycopersico

ALIGNMENTS

RESULT 1

ID	Q8BQH3	PRELIMINARY;	PRT;	505 AA.
AC	Q8BQH3;			
DT	01-JUN-2001 (TREMBLrel. 17, Created)			
DT	01-JUN-2001 (TREMBLrel. 17, Last sequence update)			
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)			
DE	Hypothetical protein (CaMKK alpha protein)			
DE	(Calcium/calmodulin-dependent protein kinase 1 alpha, isoform a).			
DE	a).			
GN	DKFZP761M0423 OR CAMKK1.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Amygdala;			
RX	MEDLINE=21154917; PubMed=11230166;			
RA	Wiemann S., Weil B., Wellenreuther R., Gassenhuber J., Glassl S.,			
RA	Ansorge W., Boecker M., Bloecker H., Bauersachs S., Blum H.,			
RA	Lauber J., Duesterhoeft A., Beyer A., Koehrer K., Strack N.,			
RA	Mewes H.W., Othenwaelder B., Obermaier B., Tampe J., Heubner D.,			
RA	Wambutt R., Korn B., Klein M., Poustka A.;			
RA	"Towards a Catalog of Human Genes and Proteins: Sequencing and			
RT	Analysis of 500 Novel Complete Protein Coding Human cDNAs.";			
RL	Genome Res. 11:422-435 (2001).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Brain;			
RA	Tascadda F., Carra S., Harvey M., Barden N.;			
RT	"Characterization of human CaMKK alpha gene structure.";			
RL	Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Brain;			
RX	MEDLINE=22388257; PubMed=12477932;			
RA	Straussberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,			

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.E., Scheetz T.E.,
 RA Brownstein M.J., Uedini T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Kzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.B.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Strausberg R.;
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DR EMBL; AL136576; CAB66511.1; -;
 DR EMBL; AF425232; AN37386.1; -;
 DR EMBL; AF425301; AN37387.1; -;
 DR EMBL; BC043487; AAH43487.1; -;
 DR HSSP; Q63450; 1A06.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR002290; Ser_thr_pkinase.
 DR InterPro; IPR008271; Ser_thr_pkinase.
 DR Pfam; PF00069; pkinase; 1.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00220; S_TKC; 1.
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE; PS00011; PROTEIN KINASE DOM; 1.
 DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
 KW Hypothetical protein; ATP-binding; Kinase;
 KW Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 505 AA; 55735 MW; 92A055D20E487C86 CRC64;
 Query Match 99.7%; Score 2626; DB 4; Length 505;
 Best Local Similarity 99.8%; Pred. No. 3e-204;
 Matches 504; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MEGGPVCCODPRAELVERVAADVTHLEADGGPEPTRNGVDPPPARAASVIPGSTSR 60
 DB 1 MEGGPVCCODPRAELVERVAADVTHLEADGGPEPTRNGVDPPPARAASVIPGSTSR 60
 QY 61 LLPARPSLSARKLSLOERPAGSYLEAAGPYATGTPASHISPRAWRRPTIESHHVAISDAE 120
 DB 61 LLPARPSLSARKLSLOERPAGSYLEAAGPYATGTPASHISPRAWRRPTIESHHVAISDAE 120
 QY 121 DCVOLNOYKQLQSEIGKAGYGVRLAYNESDRHYAMKVLKKLLKQYGFPRPPRGSG 180
 DB 121 DCVOLNOYKQLQSEIGKAGYGVRLAYNESDRHYAMKVLKKLLKQYGFPRPPRGSG 180
 QY 181 AAGGPAKQLPLERVYQETAILKLDHNVVKLIEVLDDPAEDNLYLFDLLRKGPMVE 240
 DB 181 AAGGPAKQLPLERVYQETAILKLDHNVVKLIEVLDDPAEDNLYLFDLLRKGPMVE 240
 QY 241 VPCDKPSEEQARLYLRDVLGLYLELHCQKIVHRDIKPSNLLGDDGHVKIADFGVSNQF 300
 DB 241 VPCDKPSEEQARLYLRDVLGLYLELHCQKIVHRDIKPSNLLGDDGHVKIADFGVSNQF 300
 QY 301 EGNDALQSLSTAGTAPFAFMAPEAISDSGSGKALDVWATGVTLYCFYVKGKCPFIIDFILA 360
 DB 301 EGNDALQSLSTAGTAPFAFMAPEAISDSGSGKALDVWATGVTLYCFYVKGKCPFIIDFILA 360

QY 361 LHRKIKNEPVVPEEPISEELKDLILKMLDKNPETRIGVDPDIKLHPWVTKNGEPLPSE 420
 DB 361 LHRKIKNEPVVPEEPISEELKDLILKMLDKNPETRIGVDPDIKLHPWVTKNGEPLPSE 420
 QY 421 EEHCVVVEVEGKSVRLIPSWTIVLVKSMRLKRSGFNPPFPQARRERSMSAPGNL 480
 DB 421 EEHCVVVEVEGKSVRLIPSWTIVLVKSMRLKRSGFNPPFPQARRERSMSAPGNL 480
 QY 481 LVKEGFGGCKSPELPGVQDEAAS 505
 DB 481 LVKEGFGGCKSPELPGVQDEAAS 505
 RESULT 2
 Q8N5S9 PRELIMINARY; PRT; 520 AA.
 AC Q8N5S9;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Similar to hypothetical protein DKFZp761M0423.
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain, and Lung;
 RA Strausberg R.;
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC031647; AAH31647.1; -;
 DR Genew; HGNC:1469; CAMKK1.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR002290; Ser_thr_pkinase.
 DR InterPro; IPR008271; Ser_thr_pkinase.
 DR InterPro; IPR001245; Tyr_pkinase.
 DR Pfam; PF00069; pkinase; 1.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00220; S_TKC; 1.
 DR SMART; SM00219; TYK; 1.
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE; PS00011; PROTEIN KINASE DOM; 1.
 DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
 KW Hypothetical protein; ATP-binding; Transferase.
 SQ SEQUENCE 520 AA; 57451 MW; 44B21EC1F25420F4 CRC64;
 Query Match 93.8%; Score 2470; DB 4; Length 520;
 Best Local Similarity 92.3%; Pred. No. 1.4e-191;
 Matches 480; Conservative 0; Mismatches 2; Indels 38; Gaps 1;
 QY 1 MEGGPVCCODPRAELVERVAADVTHLEADGGPEPTRNGVDPPPARAASVIPGSTSR 60
 DB 1 MEGGPVCCODPRAELVERVAADVTHLEADGGPEPTRNGVDPPPARAASVIPGSTSR 60
 QY 61 LLPARPSLSARKLSLOERPAGSYLEAAGPYATGTPASHISPRAWRRPTIESHHVAISDAE 120
 DB 61 LLPARPSLSARKLSLOERPAGSYLEAAGPYATGTPASHISPRAWRRPTIESHHVAISDAE 120
 QY 121 DCVOLNOYKQLQSEIGKAGYGVRLAYNESDRHYAMKVLKKLLKQYGFPRPPRGSG 180
 DB 121 DCVOLNOYKQLQSEIGKAGYGVRLAYNESDRHYAMKVLKKLLKQYGFPRPPRGSG 180
 QY 181 AAGGPAKQLPLERVYQETAILKLDHNVVKLIEVLDDPAEDNLYLFDLLRKGPMVE 228
 DB 181 AAGGPAKQLPLERVYQETAILKLDHNVVKLIEVLDDPAEDNLYLFDLLRKGPMVE 228
 QY 229 -----VFLLRKGPMVEVPCDKPFSEEQARLYLRDVL 262


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Db      241 STNIAKPHSLPSEQSGTWAARKSVFLLRKGVMVPCDKPPSEQEARLYRUVILG 300
Qy      263 LEYLHCQKIVHRDIKPSNLLGDDGHVKIADFGVSNQFEGNDQAQLSSTAGTAPAFMAPEAI 322
Db      301 LEYLHCQKIVHRDIKPSNLLGDDGHVKIADFGVSNQFEGNDQAQLSSTAGTAPAFMAPEAI 360
Qy      323 SDSGQSGKALDVMWATGVTLYCFYVYKCPFIDDFILALHKKIKNEPVPVPEEPISEEL 382
Db      361 SDSGQSGKALDVMWATGVTLYCFYVYKCPFIDDFILALHKKIKNEPVPVPEEPISEEL 420
Qy      383 KDLILKMLDKNPETRIGVDPDKLHPWVTKNGEELPSEEEHCSVVVTEGEVKNSVRLIP 442
Db      421 KDLILKMLDKNPETRIGVDPDKLHPWVTKNGEELPSEEEHCSVVVTEGEVKNSVRLIP 480
Qy      443 SWTTVILVKMLRKRSFGNPFEPQARRERSMSAPGNLLV 482
Db      481 SWTTVILVKMLRKRSFGNPFEPQARRERSMSAPGNLLV 520

RESULT 3
P97756
ID      P97756 PRELIMINARY; PRT; 505 AA.
AC      P97756;
DT      01-MAY-1997 (TrEMBLrel. 03, Created)
DT      01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT      01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE      CA2+/calmodulin-dependent protein kinase IV kinase isoform.
OS      Rattus norvegicus (Rat).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX      NCBI_TaxID=10116;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=96425004; PubMed=8827455;
RA      Okuno S., Kitani T., Fujisawa H.;
RT      Evidence for the existence of Ca2+/calmodulin-dependent protein
RT      kinase IV kinase isoforms in rat brain.
RL      J. Biochem. 119:1176-1181(1996).
RN      [2]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Brain;
RA      Fujisawa H., Okuno S.;
RL      Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
CC      -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR      EMBL; S83194; AAB46910.1; -.
DR      EMBL; AB023658; BAA75246.1; -.
DR      HSP; O63450; 1A06
DR      GO; GO:0005524; F:ATP binding; IEA.
DR      GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR      GO; GO:0016740; F:transferase activity; IEA.
DR      GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR      InterPro; IPR000719; Prot kinase.
DR      InterPro; IPR002290; Ser_thr_kinase.
DR      InterPro; IPR008271; Ser_thr_pkin_AS.
DR      Pfam; PF00069; pkinase; 1.
DR      ProDom; PD00001; Prot kinase; 1.
DR      SMART; SM00220; S_TK; 1.
DR      PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR      PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR      PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW      ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ      SEQUENCE 505 AA; 55907 MW; 6B268780AC9B67E1 CRC64;

Query Match
Best Local Similarity 93.7%; Score 2468; DB 11; Length 505;
Matches 472; Conservative 11; Mismatches 22; Indels 0; Gaps 0;

Qy      1 MEGGPAVCCQDPRAELVERVAIDVTHLEADGGPEPTNGVDPPPPRARAASVIGSSTR 60
Db      1 MERSFAVCCQDPRAELVERVAISVAHLEAEAGPEPASGVDPPPPRARAASVIGSASR 60
Qy      61 LLPAPRSLSARKLSQERPAQSLEAQAGFYATGPASHISPRAWRRPTIESHHVAISDAE 120

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Db      61 PTPVRPSLSARKFSQERPAQSLEAQAGFYATGPASHISPRAWRRPTIESHHVAISDAE 120
Qy      121 DCVOLNQYKLOSEICKGAYGVVRLAYNESEDRHYAMKVLSSKKLLKQYGFRRPPRRSQ 180
Db      121 DCVOLNQYKLOSEICKGAYGVVRLAYNEREDRHYAMKVLSSKKLLKQYGFRRPPRRSQ 180
Qy      181 AAGGPAKQLPLBRVQOEIAILKKLDHVNKKIEVLDDPAEDNLYLVFLLRKGPMVE 240
Db      181 AAGGPAKQLPLBRVQOEIAILKKLDHVNKKIEVLDDPAEDNLYLVFLLRKGPMVE 240
Qy      241 VPCDKPSEEOARLYRDLVILGLEVYLCQKIVHRDIKPSNLLGDDGHVKIADFGVSNQF 300
Db      241 VPCDKPSEEOARLYRDLVILGLEVYLCQKIVHRDIKPSNLLGDDGHVKIADFGVSNQF 300
Qy      301 EGNDQAQLSSTAGTAPAFMAPEAISDSGQSGKALDVMWATGVTLYCFYVYKCPFIDDFILA 360
Db      301 EGNDQAQLSSTAGTAPAFMAPEAISDSGQSGKALDVMWATGVTLYCFYVYKCPFIDDFILA 360
Qy      361 LHRKIKNEPVVPEEPISEELKDLILKMLDKNPETRIGVDPDKLHPWVTKNGEELPSE 420
Db      361 LHRKIKNEPVVPEEPISEELKDLILKMLDKNPETRIGVDPDKLHPWVTKNGEELPSE 420
Qy      421 EEHCSVVTEGEVKNSVRLIPSWTTVILVKMLRKRSFGNPFEPQARRERSMSAPGNL 480
Db      421 EEHCSVVTEGEVKNSVRLIPSWTTVILVKMLRKRSFGNPFEPQARRERSMSAPGNL 480
Qy      481 LVKSGFGGKSPGLPGVQDEAAS 505
Db      481 LVKSGFGGKSPGLPGVQDEAAS 505

RESULT 4
Q8VBY2
ID      Q8VBY2 PRELIMINARY; PRT; 505 AA.
AC      Q8VBY2;
DT      01-MAR-2002 (TrEMBLrel. 20, Created)
DT      01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT      01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE      Calcium/calmodulin-dependent protein kinase alpha (Similar to
DE      calcium/calmodulin-dependent protein kinase alpha 1, alpha).
GN      CAMKK1.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=129/SvJ;
RA      Blaesser F., Ho N., Chatila T.A.;
RL      "Genomic Organization of Murine CamKKalpha Gene.";
RL      Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
RN      [2]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Salivary gland;
RA      Strausberg R.;
RL      Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
CC      -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR      EMBL; AF461706; AAL67849.1; -.
DR      EMBL; AF461702; AAL67849.1; JOINED.
DR      EMBL; AF461703; AAL67849.1; JOINED.
DR      EMBL; AF461704; AAL67849.1; JOINED.
DR      EMBL; AF461705; AAL67849.1; JOINED.
DR      EMBL; BC017529; AAL17529.1; -.
DR      MGD; MGI:1891766; Camkk1.
DR      GO; GO:0005524; F:ATP binding; IEA.
DR      GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR      GO; GO:0016740; F:transferase activity; IEA.
DR      GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR      InterPro; IPR000719; Prot kinase.
DR      InterPro; IPR002290; Ser_thr_pkinase.
DR      InterPro; IPR008271; Ser_thr_pkin_AS.
DR      Pfam; PF00069; pkinase; 1.

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OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20023572; PubMed=10560916;
RA Lawson N.D., Zain M., Zibello T., Picciotto M.R., Nairn A.C.,
RA Belziner N.;
RT "Modulation of a calcium/calmodulin-dependent protein kinase cascade
RT by retinoic acid during neutrophil maturation.";
RL Exp. Hematol. 27:1682-1690(1999).
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL: AF117384; AAF08348.1; -.
DR HSSP: Q63450; 1A06.
DR MGD: MGI:1891766; Camkkl.
DR GO: GO:0005524; F:ATP binding; IEA.
DR GO: GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO: GO:0016740; F:transferase activity; IEA.
DR GO: GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR002290; Ser_thr_kinase.
DR InterPro: IPR008271; Ser_thr_pkin_AS.
DR Pfam: PF00069; pkinase; 1.
DR ProDom: PD000001; Prot_kinase; 1.
DR SMART: SM00220; S_TKc; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 505 AA; 55879 MW; 31CB9588C903BBDC CRC64;

Query Match 91.8%; Score 2419; DB 11; Length 505;
Best Local Similarity 91.3%; Pred. No. 1.8e-187;
Matches 461; Conservative 15; Mismatches 29; Indels 0; Gaps 0;

QY 1 MEGPAVCCQDPAELVERVAADIVTHLEADGGPEPTRNGVDPPPRARAAVIPGSTR 60
DB 1 MESGPAVCCQDPAELVDRAVAINVAHLEADEGEPARNGVDPPPRARAAVIPGSASR 60
QY 61 LLPARPSLSARKLSLOERPAGSYLEAQAQVATGPASHISPRAMRRPTIESHHVAISDAE 120
DB 61 PTPVRPXLRSKFSLSQEPXGKCLGAQVGYSTGPASHMCPRSRRPTIESHRVAISDTE 120
QY 121 DCVOLNOYKLOSEIGKGAYGVVRLAYNESEDHRYAMKVLKSKLLKQYGFPRRPPRGSQ 180
DB 121 DCVOLNQYKLOSEIGKGAYGVVRLAYNESEDHRYAMKVLKSKLLKQYGFPRRPPRGSQ 180
QY 181 AAQGGPAKQLPLERVYQEIAILKKLDHNVNKKLIEVLDDPAEDNLYLVFDLLRKGPMVE 240
DB 181 ATQGGPAKQLPLERVYHDIALLKKLDHNVNKKLIEVLDDPAEDNLYLVFDLLRKGPMVE 240
QY 241 VPCDKPFSEQARLYLRDVLVGLVHCQKIVHRDIKPSNLLLGDDGHVKIADFGVSNQF 300
DB 241 VPCDKPFPEQARLYLRDILGLVHCQKIVHRDIKPSNLLLGDDGHVKIADFGVSNQF 300
QY 301 EGNDAQLSSTAGTAFMAPEAISDSGQSGKALDVWATGVTLVCFVYKCPFFIDDFILA 360
DB 301 EGNDAQLSSTAGTAFMAPEAISDSGQSGKALDVWATGVTLVCFVYKCPFFIDDFILA 360
QY 361 LHRKIKNEPVVFPPEPEISEELKOLILKMLDKNPETRIGVDPDKLHPWTKNGEPLPSE 420
DB 361 LHRKIKNEAVVFPPEPEVSEDSKOLILKMLDKNPETRIGVSDIKLHPWTKHGEPIPSE 420
QY 421 EHCVCVVEVTEGEVKNVRLIPSWTTVILVKSMMLKRSFGNPFEPQARREERMSAPGNL 480
DB 421 EHCVCVVEVTEEVKNVRLIPSWTTVILVKSMMLKRSFGNPFEPQARREERMSAPGSL 480
QY 481 LVKEGFGEGGCKSPQLPGVQDEAAS 505
DB 481 LMKEGCGEGGCKSPQLPGVQDEAAS 505

RESULT 7
Q8AYR1 PRELIMINARY; PRT; 523 AA.
ID Q8AYR1
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AC Q8AYR1;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Calcium/calmodulin-dependent protein kinase kinase.
DE CAM-KK.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Saneyoshi T., Kume S., Mikoshiba K.;
RT "calcium/calmodulin-dependent protein kinase kinase."
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB083001; BAC19849.1; -.
DR GO: GO:0005524; F:ATP binding; IEA.
DR GO: GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO: GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO: GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR002290; Ser_thr_kinase.
DR InterPro: IPR008271; Ser_thr_pkin_AS.
DR InterPro: IPR001245; Tyr_pkinase.
DR Pfam: PF00069; pkinase; 1.
DR ProDom: PD000001; Prot_kinase; 1.
DR SMART: SM00220; S_TKc; 1.
DR SMART: SM00219; TyrKc; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW Kinase.
SQ SEQUENCE 523 AA; 58653 MW; 33ACDF0EE4682B0A CRC64;

Query Match 69.6%; Score 1834; DB 13; Length 523;
Best Local Similarity 69.7%; Pred. No. 5.3e-140;
Matches 361; Conservative 56; Mismatches 77; Indels 24; Gaps 5;

QY 6 AVCCQDPAELVERVAADIV-----THLEADG-----GPEPTRNGVDPPPRARA 50
DB 12 SVPSQDSQSELAAERVAALVEEECCQAPERMSDDMDGLKNHCMSSETSQDFLSQEQRD 71
QY 51 ASVTGSTRLLPARPSLSARKLSLOERPAGSYLEAQ---AGPYATGPASHISPRAMRRP 107
DB 72 LSTFORASS-----RPSLSNRKFSLOERPSSGCLPSHNLAYGPYATGPASHISPRIVRRP 126
QY 108 TIESHHVAISDAEDCVOLNOYKLOSEIGKGAYGVVRLAYNESEDHRYAMKVLKSKLLKQ 167
DB 127 TIESNRVSISSDDCVQLNQYKLOSEIGKGSYGVVKKLAYNSDDDKYAMKVLKSKLLKQ 186
QY 168 YGFRPRPPRGSQAQGGPAKQLPLERVYQEIAILKKLDHNVNKKLIEVLDDPAEDNLY 227
DB 187 YGFRPRPPRSGTKSGDQTKPMAPLDRVYQEIALLKKLDHNVNKKLIEVLDDPAEDNLY 246
QY 228 LVFDLLRKGPMVVPCKDPFSEQARLYLRDVLVGLVHCQKIVHRDIKPSNLLLGDDG 287
DB 247 MVFDLLRKGPMVVPSEHPFVEDQARVYFRDVLVGLVGLVHCQKIVHRDIKPSNLLVGDDG 306
QY 288 HVKTIADFGVSNQFNGNDQAQLSSTAGTAFMAPEAISDSGQSGKALDVWATGVTLVCFV 347
DB 307 HIKTIADFGVSNQFNGNDALLSSTAGTAFMAPELTAQSGQSGKALDVWATGVTLVCFV 366
QY 348 YGKCPFFIDDFILALHRKIKNEPVVFPPEPEISEELKOLILKMLDKNPETRIGVDPDKLHP 407
DB 367 FGKCPFWDEFILTLHNKIKYKPFVEFPPEPSISNDLKOLILKMLDKKPEDRLSVPEIKVHP 426
QY 408 WTKNGEPLPSEBEHCVCVVEVTEGEVKNVRLIPSWTTVILVKSMMLKRSFGNPFEPQ 467
DB 427 WVTNRGEDHLPLEEHECHTIVEVTEEVKNVSKLIPSLTTLVKAMLRKRSFGNPF-CA 485
QY 468 PREERSNSAPGNLAVKEGFGEGGCKSPQLPGVQDEAAS 505
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Db 486 RRERSMSAPGNLLIKQVSEVAKSDLPDVEDEGTS 523
RESULT 8
Q8WY04 PRELIMINARY; PRT; 541 AA.
AC Q8WY04;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE CAMKK beta 1 isoform (Similar to calcium/calmodulin-dependent protein
DE kinase kinase 2, beta).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DE EMBL; AF321387; AAU37217.1; -.
DR EMBL; BC026060; AAH26060.1; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR Pfam; PF00069; pkinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00011; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 541 AA; 59587 MW; 3D3AC0943A7D7941 CRC64;

Query Match 58.4%; Score 1537.5; DB 4; Length 541;
Best Local Similarity 62.0%; Pred. No. 6.1e-116;
Matches 300; Conservative 79; Mismatches 74; Indels 31; Gaps 5;

QY 30 EADGPEPTRNGVDPPPRARAASVPGSTSRLLPARPSLSARKLSLQER-----PAGSYL 84
Db 75 EADGQEVF-----LDSSGSQ---ARPHLSGRKLSLQERSQGLAGGSL 115

QY 85 EAQAG-----PYATGPASHISPAWRPRTIESHHVAISDAEDCVQLNKLQSEIGKGA 138
Db 116 DMNGRCICPSLPSPVSSPQSPRLPRPTVESHHVSIITGMQDCVQLNKLQSEIGKGS 175

QY 139 YGVVRLAYNESEDRHYAMKVLKSKLLKQYGFRRPRPRGCSQAQGPAKQLLPLERVYQ 198
Db 176 YGVVVKLAYNENDNTYYAMKVLKSKLLKQYGFRRPRPRGCSQAQGPAKQLLPLERVYQ 235

QY 199 ETAILKKLDHNVVVKLTIEVDDPAEDNLVLFVLLRKGPMVEVPCDKPFSEEQARLYLRD 258
Db 236 ETAILKKLDHNVVVKLTIEVDDPAEDNLVLFVLLRKGPMVEVPTLKPLSEDAQRFYQD 295

QY 259 VIILGLEYLHCQKIVHRDIKPSNLLLDGDDHVKVTADFGVSNQPGNDAQLSSTAGTAFMA 318
Db 296 LIRGIEYLHYQKIIHRDIKPSNLLLVGDDGHIKTADEFGVSNFEGSDALLSNTVGTAFMA 355

QY 319 PEALSDSGSQSGKALDVMATGVTLYCFYVGKCPFFIDFTLALHRKIKNEPVVFPPEPEI 378
Db 356 PESLSETRKIFSGKALDVMATGVTLYCFYVGKCPFFIDFTLALHRKIKNEPVVFPPEPEI 415
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QY 379 SEELKDLILKMLDKNPETRIGVDPDILKHPMTVKNGEPLPSEBEHCSVVEVTGEVKNV 438
Db 416 AEDLKDLITRMLDKNPESRIVVPEIKLHPMTVKNGEPLPSEBEHCSVVEVTGEVKNV 475

QY 439 RLIPSWTTVILVKSLMRKSGFNGFPFQARREERSMSAPGNLLIKQVSEVAKSDLPDVE 498
Db 476 KHIPSLATVILVKTMIRKSGFNGPFE-GSRREERSLSAPGNLLIKQVSEVAKSDLPDVE 534

QY 499 QDEE 502
Db 535 GEEE 538

RESULT 9
Q8IU03 PRELIMINARY; PRT; 541 AA.
AC Q8IU03;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Ca2+/calmodulin-dependent protein kinase kinase beta-3.
GN CAMKK BETA-3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Ishikawa Y., Tokumitsu H., Inuzuka H., Murata-Hori M., Hosoya H.,
RA Kobayashi R.;
RT "Identification and characterization of novel components of
RT Ca2+/calmodulin-dependent protein kinase cascade in HeLa cells.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA MEDLINE-21391903; PubMed-11395482;
RA Hsu L.S., Chen G.D., Lee L.S., Chi C.W., Cheng J.F., Chen J.Y.;
RT "Human Ca2+/calmodulin-dependent protein kinase kinase beta gene
RT encodes multiple isoforms that display distinct kinase activity.";
RL J. Biol. Chem. 276:31113-31123 (2001).
DR EMBL; AB081336; BAC19840.1; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; pkinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00011; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
KW Kinase.
SQ SEQUENCE 541 AA; 59601 MW; D9A56C3D780C0DDE CRC64;

Query Match 58.3%; Score 1536; DB 4; Length 541;
Best Local Similarity 65.1%; Pred. No. 8.1e-116;
Matches 293; Conservative 77; Mismatches 68; Indels 12; Gaps 3;

QY 64 ARPSLSARKLSLQER-----PAGSYLEAQAQ-----PYATGPASHISPAWRPRTIESH 112
Db 90 ARPHLSGRKLSLQERSQGLAGGSLDMNGRCICPSLPSPVSSPQSPRLPRPTVESH 149

QY 113 HVAISDAEDCVQLNKLQSEIGKGA YGVVRLAYNESEDRHYAMKVLKSKLLKQYGFRR 172
Db 150 HVSITGMQDCVQLNKLQSEIGKGS YGVVVKLAYNENDNTYYAMKVLKSKLLKQYGFRR 209

QY 173 RPPPRGSAQAGGPAPKQLLPLERVYQETAILKKLDHNVVVKLTIEVDDPAEDNLVLF 232
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Db      210 RPPRGTRPAPGGCIQPRGPIEQVYQETALIKLKDHPNVVKLVFVLDNEDHLYMWTEL 269
Qy      233 LRKGFVMEVPCDKPFPSEQARLYLRDVLGLGYLHCQKIHRDIKPSNLLGLDGDGHVXIA 292
Db      270 VNQGFMVEVPTLKLPSLSEDOARFYFDLKGIEYLHYQKIHRDIKPSNLLVGEDGHXIA 329
Qy      293 DFGVSNQFEGNDAOLSSDTAGTAPAFNAPEAISDSGQSGKALDVWATGVTLYCFVYGKCP 352
Db      330 DFGVSNQFEGNDAOLSSDTAGTAPAFNAPEAISDSGQSGKALDVWATGVTLYCFVYGKCP 389
Qy      353 FIDDFILALHKKIKNEPVVFPPEPRISBELKDLILKMDKNPETRIGVDPDIKLHPWTKN 412
Db      390 FMDERIMCLHSKIKSQALEFFDQPIADLKDILTRMLDKNPESIVVPEIKLHPWTRH 449
Qy      413 GEELPSPSEEHCSVVVEGEVKSVRILPSTVTVILYKSMRLKRSFGNPFEPQARRER 472
Db      450 GAELPSPSEENCTLVETVEEVENSVKHPSLATVILVKTMRKRSFGNPFEPQARRER 508
Qy      473 SMSAPGNLLVKEGFGEGCKSPELPGVQDE 502
Db      509 SLSAPGNLLTKQSGSDNLQGTDPVPVGE 538

RESULT 10
O94883
ID O94883 PRELIMINARY; PRT; 557 AA.
AC O94883;
TX MEDLINE=99087487; PubMed=9872452;
RA Nagase T., Ishikawa K., Suyama M., Kikuno R., Miyajima N., Tanaka A.,
RA Kotani H., Nomura N., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. XI.
RT The complete sequences of 100 new cDNA clones from brain which code
RT for large proteins in vitro.";
RL DNA Res. 5:277-286(1998).
DR EMBL; AB018330; BAA34507.2; -.
DR HSSP; Q63450; 1A06.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR Pfam; PF00069; kinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00219; TyrK; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Hypothetical protein; ATP-binding; Transferase.
FT NON TER 1
SQ SEQUENCE 557 AA; 61473 MW; 63876A1877DF9224 CRC64;

Query Match 57.9%; Score 1525.5; DB 4; Length 557;
Best Local Similarity 62.0%; Pred. No. 6e-115;
Matches 299; Conservative 77; Mismatches 75; Indels 31; Gaps 5;

Qy      30 EADGCPETRNGVDPPPPARAASVIGPSTRLPARPSLSARKLSLQER-----PAGSYL 84

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Db      76 EADGQEV-----LDSSGQ---ARPHLSGRKLSQERSQGLAAGSL 116
Qy      85 EAQAG-----PYATGPASHISPRARRPTTIESHHVAISDAEDCVQLMQYKLSQSIGKA 138
Db      117 DMNGRCICPSLPYSPVSPQSPRLPRPTVESHVSVITGMQDCVQLNQYTLKDEIGKS 176
Qy      139 YGVRLAYNESSEDRHYAMKVLKKKLLKQYQFPPRRPPRGSQAAGGPAKQLLPVYVQ 198
Db      177 YGVVKLAYNENDNTYAMKVLKKKLIQAGFPFRPPRGRTRPAPGGCIQPRGPIEQVYQ 236
Qy      199 ETAILKLDHNVVKLIEVLDDPAEDNLVYFDILLRKGPVMEVPCDKPSEQARLYLRD 258
Db      237 ETAILKLDHNVVKLIEVLDDPNEEDHLYMVFELVNOQFVMEVPTLKLPSLSEDOARFYQD 296
Qy      259 VILGLYHLHCQKIHRDIKPSNLLGLDGDGHVKIADFGVSNQFEGNDAOLSSDTAGTAPAFNA 318
Db      297 LIKGIEYLHYQKIHRDIKPSNLLVGEDGHKIAIDFGVSNFEKSDALLSNTVGTAPAFNA 356
Qy      319 PEAISDSGQSGKALDVWATGVTLYCFVYGKCPFIDDFILALHKKIKNEPVVFPPEPR 378
Db      357 PESLSETRKIFSGKALDVWAMGVTLVYCFVQCPFMDERIMCLHSKIKSQALEFPDQDI 416
Qy      379 SEELKDLILKMDKNPETRIGVDPDIKLHPWTKNGEELPSEEHCSVVVEGEVKS 438
Db      417 AEDLKDLITRMLDKNPESIVVPEIKLHPWTRHGAELPSEDEENCTLVETVEEVENS 476
Qy      439 RLIPSTVTVILYKSMRLKRSFGNPFEPQARRERSMSAPGNLLVKEGFGEGCKSPELPGV 498
Db      477 KHIFSLATVILVKTMRKRSFGNPFEPQARRERSMSAPGNLLVKEGFGEGCKSPELPGV 535
Qy      499 QE 500
Db      536 KK 537

RESULT 11
Q8QZT7
ID Q8QZT7 PRELIMINARY; PRT; 541 AA.
AC Q8QZT7;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Similar to Ca+/calmodulin-dependent protein kinase beta (CaM-
DE kinase kinase beta).
GN CAMKK2 OR 6330570N16RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; BC023103; AAH23103.1; -.
DR MGD; MGI:2444812; CamkK2.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR Pfam; PF00069; kinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 541 AA; 59616 MW; FEB2385A4D793FF2 CRC64;

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Query Match 57.9%; Score 1525; DB 11; Length 541;
Best Local Similarity 60.1%; Pred. No. 6.3e-115;
Matches 300; Conservative 79; Mismatches 70; Indels 50; Gaps 7;
SQ SEQUENCE 533 AA; 5885 MW; 55B830B6EE4B678D CRC64;

QY 36 EPTRENGV-----DPPPRARAASVIFGSTRRLP-----ARPSLSARKLSLQERPAGS 82
DB 58 EPGR-GVDNLNLRDQPEA-----DQELPLEASDPESRSPPLSGRWSLQE----- 102
QY 83 YLEAQAGP-----YATGPASHISPRAWRPRTTIESHVHVAISDAEDCV 123
DB 103 --PSOGGPASSNSLDMNGRCICPSLSPASSPQSPRPMPRPRTVESHHSVITGLQDCV 160
QY 124 QLNQYKLSQSIGKAGYGVVRLAYNESDRHYAMKVLKSKLLKQYGFPRPPRPGSQAQ 183
DB 161 QLNQYTLKDEIGKSGYGVVRLAYNENDNTYYAMKVLKSKLLKQAGFFRRPPRGARPAP 220
QY 184 GGPAKQLPLERYVQETAILKLDHNVVVKLIEVLDDPAEDNLYLVFDLLKRGFVMEVPC 243
DB 221 GGCIQPRGPTEQVYQETAILKLDHNVVVKLIEVLDDPNEDHLYVMVFELVQGFVMEVPT 280
QY 244 DKPFSEQARLYLRDVLGLYELHCQKIVHRDIKPSNLLGDDGHVKIADFGVSNQFEGN 303
DB 281 LKPLSDQARFYQDLTKGTEYHLYQKIIHRDIKPSNLLGEGDGHKIAIDFGVSNFEFGS 340
QY 304 DAQLSSTAGTAPAFWAPPAISDSGQSFSGKALDVWATGVTLYCFVYGKCPFIDDFILALHR 363
DB 341 DALLSVNTVGTAPAFAPESLSSETRKIFSGKALDVWAMGVTLVCFVFGCPFMDEIRIMCLHS 400
QY 364 KIRNEPVVFPPEPEISSELKDLILKMDKNPETRIGVPDIKLPWVTNKGEEPLPSEEH 423
DB 401 KIKSQALEFPDQDIAEDLKDLITMLDKNPESRIVVPEIKLHPWVTRHGAELPSEDEN 460
QY 424 CSVVVEVTEGVKNSVRLIPSWTVVILVKSMLRKSFGNPFEPQARREERSMSAPGNLLVK 483
DB 461 CTLVEVTEEVENSXVHPSLATVILVKTMRKSGFNPFEGSRREERSLSPGNLLTK 519
QY 484 EGFEGGKSPELPGVQDE 502
DB 520 QGSEDSRGPPEAPVGEER 538

RESULT 12

Q96RR3 PRELIMINARY; PRT; 533 AA.
ID Q96RR3
AC Q96RR3
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Calcium/calmodulin-dependent protein kinase b2.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21391903; PubMed=11395482;
RA Hsu L.S., Chen G.D., Lee L.S., Chi C.W., Cheng J.F., Chen J.Y.;
RT "Human Ca2+/Calmodulin-dependent Protein Kinase beta Gene
RT Encodes Multiple Isoforms That Display Distinct Kinase Activity.";
RL J. Biol. Chem. 276:31113-31123(2001).
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; AF287631; AAK64601.1; -;
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004574; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR002290; Ser Thr pkinase.
DR InterPro; IPR008271; Ser Thr pkinase.
DR Pfam; PF00069; pkinase; I.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

RESULT 13

Q96RR4 PRELIMINARY; PRT; 588 AA.
ID Q96RR4
AC Q96RR4
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Calcium/calmodulin-dependent protein kinase b1.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21391903; PubMed=11395482;
RA Hsu L.S., Chen G.D., Lee L.S., Chi C.W., Cheng J.F., Chen J.Y.;
RT "Human Ca2+/Calmodulin-dependent Protein Kinase beta Gene
RT Encodes Multiple Isoforms That Display Distinct Kinase Activity.";
RL J. Biol. Chem. 276:31113-31123(2001).
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; AF287630; AAK64600.1; -;
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004574; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR002290; Ser Thr pkinase.
DR InterPro; IPR008271; Ser Thr pkinase.
DR Pfam; PF00069; pkinase; I.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKC; 1.


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DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 588 AA; 64731 MW; D4C4583561341166 CRC64;

Query Match
Best Local Similarity 57.6%; Score 1518.5; DB 4; Length 588;
Matches 295; Conservative 75; Mismatches 65; Indels 31; Gaps 5;

QY 30 EADGGEPTNRNGVDPPEPRARAASVPGSTSRLLPAPESLSARKLSQER-----PAGSVYL 84
DB 75 EADGGEVP-----LDSSGQ---ARPHLSGRKLSQERSQGGLAAGSL 115
QY 85 EAQAG-----PYATGPASHISPRAWRPTIESHVAISDAEDCVOLNQYKLQSEIGKA 138
DB 116 DMNGRCICPSLPYSPVSSPQSPLRPRTVESHHVSIITGMQDCVOLNQYTLKDEIGKS 175
QY 139 YGVVRLAYNESEDRHYAMKVLKSKLLKQYGPFRPPRGSOAAGGPAKOLLPLERVYQ 198
DB 176 YGVVRLAYNESEDRHYAMKVLKSKLLKQYGPFRPPRGSOAAGGPAKOLLPLERVYQ 235
QY 199 ETAILKLDHVNVMKLIIEVLDPAEDNLVLPDRLKRGPMVEPCDKPFSEQARLYLRD 258
DB 236 ETAILKLDHVNVMKLIIEVLDPAEDNLVLPDRLKRGPMVEPCDKPFSEQARLYLRD 295
QY 259 VILGLEYLHCQKIVHRDIKPSNLLGDDGHVFIADFGVSNQFEGNDAQLSSTAGTPAFMA 318
DB 296 LIKGIEYLHYQKIHRDIKPSNLLGDDGHVFIADFGVSNQFEGNDAQLSSTAGTPAFMA 355
QY 319 PRAISDSGOSFGSKALDVWATGTYLCFYVYKCPFDIDFILAHRKIKNEPVVFPPEEI 378
DB 356 PRAISDSGOSFGSKALDVWATGTYLCFYVYKCPFDIDFILAHRKIKNEPVVFPPEEI 415
QY 379 SEELKDLILKMLDKNPETRIQVDPDKLHPWTKNGEPLPSBEHCSSVVEVEGEVNSV 438
DB 416 AEDLKDLITRMLDKNPESILVPEIKLHPWTKNGEPLPSBEHCSSVVEVEGEVNSV 475
QY 439 RLIPSWTIVLVKSMRLKRSFGNPFEPQARREERSMSAPGNLLVKE 484
DB 476 KHIPSLATVILVTKMIRKRSFGNPFEPQARREERSMSAPGNLLVKE 520

RESULT 14
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AC Q96RP2;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Ca2+/calmodulin-dependent protein kinase beta 2.
GN CAMKK2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21391903; PubMed=11395482;
RA Hsu L.S., Chen G.D., Lee L.S., Chi C.W., Cheng J.F., Chen J.Y.;
RT "Human Ca2+/Calmodulin-dependent Protein Kinase Beta Gene
RT Encodes Multiple Isoforms That Display Distinct Kinase Activity.";
RL J. Biol. Chem. 276:31113-31123(2001).
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; AF321401; AAK91830.1; JOINED.
DR EMBL; AF321390; AAK91830.1; JOINED.
DR EMBL; AF321575; AAK91830.1; JOINED.
DR EMBL; AF321391; AAK91830.1; JOINED.
DR EMBL; AF321392; AAK91830.1; JOINED.
DR EMBL; AF321393; AAK91830.1; JOINED.
DR EMBL; AF321576; AAK91830.1; JOINED.
DR EMBL; AF321577; AAK91830.1; JOINED.
DR EMBL; AF321394; AAK91830.1; JOINED.

DR EMBL; AF321395; AAK91830.1; JOINED.
DR EMBL; AF321396; AAK91830.1; JOINED.
DR EMBL; AF321397; AAK91830.1; JOINED.
DR EMBL; AF321398; AAK91830.1; JOINED.
DR EMBL; AF321399; AAK91830.1; JOINED.
DR EMBL; AF321400; AAK91830.1; JOINED.
DR EMBL; AF321578; AAK91830.1; JOINED.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000719; Prot. kinase.
DR InterPro; IPR002290; Ser thr pkinase.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Prot. kinase; 1.
DR SMART; SM00220; S_TKc_1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 533 AA; 58899 MW; 98FAAB0FB8C4CACF CRC64;

Query Match
Best Local Similarity 57.6%; Score 1517; DB 4; Length 533;
Matches 288; Conservative 73; Mismatches 59; Indels 12; Gaps 3;

QY 64 ARPSLSARKLSQER-----PAGSVLEAQG-----PYATGPASHISPRAWRPTIESH 112
DB 90 ARPHLSGRKLSQERSQGGLAAGSLDMNGRCICPSLPYSPVSSPQSPLRPRTVESH 149
QY 113 HVAISDAEDCVOLNQYKLQSEIGKAGYGVVRLAYNESEDRHYAMKVLKSKLLKQYGFPR 172
DB 150 HVSITGMQDCVOLNQYTLKDEIGKSGYGVVRLAYNESEDRHYAMKVLKSKLLKQYGFPR 209
QY 173 RPPRGSOAAGGPAKOLLPLERVYQETAILKLDHVNVMKLIIEVLDPAEDNLVLPDL 232
DB 210 RPPRGSOAAGGPAKOLLPLERVYQETAILKLDHVNVMKLIIEVLDPAEDNLVLPDL 269
QY 233 LRKGPVMEVPCDKPFSEQARLYLRDVLGLBYLHCQKIVHRDIKPSNLLGDDGHVKT 292
DB 270 VNQGPVMEVPTLPLSEDOARFYFQDLKGIYLYQKIHRDIKPSNLLGDDGHVKT 329
QY 293 DFGVSNQFEGNDAQLSSTAGTPAFMAPEAISDSGOSFGSKALDVWATGTYLCFYVYKCP 352
DB 330 DFGVSNQFEGNDAQLSSTAGTPAFMAPEAISDSGOSFGSKALDVWATGTYLCFYVYKCP 389
QY 353 FIDDEILALHRKIKNEPVVFPPEEPISEELKDLILKMLDKNPETRIQVDPDKLHPWTKN 412
DB 390 FMDEIRIMCLSHKSKISQALEFPDQDIAEDLKDLITRMLDKNPESILVPEIKLHPWTKN 449
QY 413 GREPLPSBEHCSSVVEVEGEVNSVRLIPSWTIVLVKSMRLKRSFGNPFEPQARREER 472
DB 450 GREPLPSBEHCSSVVEVEGEVNSVRLIPSWTIVLVKSMRLKRSFGNPFEPQARREER 508
QY 473 SMSAPGNLLVKE 484
DB 509 SILSAPGNLLTKK 520

RESULT 15
Q96RP1 PRELIMINARY; PRT; 588 AA.
AC Q96RP1;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Ca2+/calmodulin-dependent protein kinase beta 1.
GN CAMKK2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 11, 2004, 22:58:23 ; Search time 1366 Seconds
(without alignments)
7813.913 Million cell updates/sec

Title: US-10-690-617-1

Perfect score: 2190
Sequence: 1 cqcqcgqgqctagctcgg.....ctcttctattcagacgct 2190

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3183909 seqs, 2436941669 residues

Total number of hits satisfying chosen parameters: 6367818

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	2190	100.0	2190	14	US-10-135-689-1	Sequence 1, Appli
2	2190	100.0	2190	17	US-10-690-617-1	Sequence 1, Appli
3	2001.6	91.4	3501	13	US-10-168-582-14	Sequence 14, Appli
4	1306.4	87.1	1337	13	US-10-333-314-39	Sequence 39, Appli
5	1636.2	74.7	2711	9	US-09-922-138-7	Sequence 7, Appli
6	1636.2	74.7	2711	17	US-10-391-364-41	Sequence 41, Appli
7	1610.2	73.5	2018	13	US-10-302-172-433	Sequence 43, Appli
8	1601.4	73.1	1611	13	US-10-092-900A-55	Sequence 55, Appli
9	1493.8	68.2	1547	13	US-10-092-900A-53	Sequence 53, Appli
10	1490.6	68.1	1683	9	US-09-922-138-9	Sequence 9, Appli
11	1490.6	68.1	1686	17	US-10-391-364-43	Sequence 43, Appli
12	1475.8	67.4	1725	13	US-10-092-900A-57	Sequence 57, Appli
13	653.6	29.8	5611	16	US-10-295-027-1138	Sequence 1138, Ap
14	651.2	29.7	4427	15	US-10-316-124-7	Sequence 7, Appli

15	651.2	29.7	4427	15	US-10-316-124-8	Sequence 8, Appli
16	651.2	29.7	4942	15	US-10-205-823-51	Sequence 51, Appl
17	651	29.7	1804	15	US-10-205-823-53	Sequence 53, Appl
18	645.6	29.5	2056	14	US-10-098-841-22	Sequence 22, Appl
19	572	26.1	731	13	US-10-296-115-20	Sequence 20, Appl
20	561.4	25.6	29629	14	US-10-315-689-3	Sequence 3, Appli
21	561.4	25.6	29629	17	US-10-690-617-3	Sequence 3, Appli
22	529.6	24.2	705	9	US-09-764-868-225	Sequence 225, App
23	529.6	24.2	705	11	US-09-764-875-182	Sequence 182, App
24	518	23.7	1927	14	US-09-098-841-23	Sequence 23, Appl
25	427.8	19.5	1652	13	US-10-425-114-26840	Sequence 26840, A
26	395.8	18.1	432	17	US-10-283-975A-947	Sequence 847, App
27	389.4	17.8	1854	18	US-09-895-298-57	Sequence 57, Appl
28	348.8	15.9	439	13	US-10-296-115-247	Sequence 247, App
29	274.6	12.5	876	13	US-09-823-245A-163	Sequence 163, App
30	262.6	12.0	491	10	US-09-918-995-1271	Sequence 1271, Ap
31	244.6	11.2	485	10	US-09-918-995-2780	Sequence 2780, Ap
32	201.2	9.2	218	9	US-09-864-761-5606	Sequence 5606, Ap
33	201	9.2	218	9	US-09-864-761-22375	Sequence 22375, A
34	142.8	6.5	288	16	US-10-305-720-1008	Sequence 1008, Ap
35	139	6.3	463	9	US-09-764-869-1603	Sequence 1603, Ap
36	139	6.3	463	15	US-10-091-504-1603	Sequence 1603, Ap
37	139	6.3	463	16	US-10-227-577-1603	Sequence 192, App
38	136.8	6.2	463	9	US-09-764-869-192	Sequence 192, App
39	136.8	6.2	463	15	US-10-091-504-192	Sequence 192, App
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C 41	114.6	5.2	529	9	US-09-954-456-1333	Sequence 1333, Ap
C 42	114.6	5.2	529	9	US-09-880-107-1390	Sequence 1390, Ap
43	113.8	5.2	1743	13	US-10-425-114-15808	Sequence 15808, A
44	110.8	5.1	1268	13	US-10-425-114-31104	Sequence 31104, A
45	106	4.8	1448	17	US-10-437-963-59393	Sequence 59393, A

ALIGNMENTS

RESULT 1

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US-10-135-689-1
; Sequence 1, Application US/10135689
; Publication No. US20020123121A1
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL000904DIV
; CURRENT APPLICATION NUMBER: US/10/135,689
; CURRENT FILING DATE: 2002-05-01
; PRIOR APPLICATION NUMBER: 60/247,031
; PRIOR FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: 09/729,995
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2190
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-135-689-1

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	Matches 2190;	Conservative	Mismatches	Indels	Gaps
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Db	1	CGCCCGCGGGCTGAGCTCGGCGATCTGGGCCCCAGCGAGCGCGTGGGGCGGGCGGGGGCG	60		
Qy	61	GGCGGGGGCGCGACAGAGCGAGTGGGGCGCCCGCGGGCCACGGACACTGTGCGCCC	120		
Db	61	GGCGGGGGCGCGACAGAGCGAGTGGGGCGCCCGCGGGCCACGGACACTGTGCGCCC	120		
Qy	121	GGCGGCCAGGTTCCCAACAAAGGCTACGCGAAGAAACCCCTTCACCTGAACCAATGAGGG	180		

Db 121 GGGGCCCGAGGTTCCCAACAAGGCTACGAGAGAACCCCTTGACTGAGCAATGAGGG 180
QY 181 GGGTCCAGCTGTCTGTGCCAGGATCTCTCGGCGAGAGCTGGTAGAAGGGGTGGCAGCCAT 240
Db 181 GGGTCCAGCTGTCTGTGCCAGGATCTCTCGGCGAGAGCTGGTAGAAGGGGTGGCAGCCAT 240
QY 241 CGATGTACTCACTTGGAGGAGGAGATGGTGGCCAGAGCTTACTAGAAACGGTGTGGA 300
Db 241 CGATGTACTCACTTGGAGGAGGAGATGGTGGCCAGAGCTTACTAGAAACGGTGTGGA 300
QY 301 CCCCCCACCAGGGCCAGAGCTGCTCTGTGATCCCTGGCAGTACTTCAAGACTGCTCCC 360
Db 301 CCCCCCACCAGGGCCAGAGCTGCTCTGTGATCCCTGGCAGTACTTCAAGACTGCTCCC 360
QY 361 AGCCGGCCCTAGCCTCTCAGCCAGGAAGCTTTCCTACAGAGCGGCCAGCAGGAAGCTA 420
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QY 421 TCTGGAGGCGAGGCTGGGCTTATGCCAGGGGCTGCCAGCACATCTCCCCCGGGC 480
Db 421 TCTGGAGGCGAGGCTGGGCTTATGCCAGGGGCTGCCAGCACATCTCCCCCGGGC 480
QY 481 CTGCGGAGGCCCCACCATCGAGTCCCCACAGCTGCCCATCTCAGATGCAGAGACTCGGT 540
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QY 541 GCAGCTGAAACAGTACAGCTGCAAGTGCAGAGTGGCAAGGGTGCCTACCGTGTGTGAG 600
Db 541 GCAGCTGAAACAGTACAGCTGCAAGTGCAGAGTGGCAAGGGTGCCTACCGTGTGTGAG 600
QY 601 GCTGGCCCTACAAAGAAAGTGAAGACAGACTATGCAATGAAAGTCTTTCRAAAGAA 660
Db 601 GCTGGCCCTACAAAGAAAGTGAAGACAGACTATGCAATGAAAGTCTTTCRAAAGAA 660
QY 661 GTTACTGAAGCAGTATGGCTTTCACAGCTGCGCTCCCCCGAGAGGGTCCCCAGGCTGCCA 720
Db 661 GTTACTGAAGCAGTATGGCTTTCACAGCTGCGCTCCCCCGAGAGGGTCCCCAGGCTGCCA 720
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Db 721 GGGAGGACGACGAGCAGCTGTGCCCCCTGGAGCGGGTGTACAGAGATTCGCTATCCT 780
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Db 781 GAAGAACTGGACCACTGAATGTGTCAAACTGATCGAGTCTCTGATGACCCAGCTGA 840
QY 841 GGACAACTCTATTGTGTGTGACCTCTTGAGAAAGGGGCCCGGTCAATGAAAGTGCCTG 900
Db 841 GGACAACTCTATTGTGTGTGACCTCTTGAGAAAGGGGCCCGGTCAATGAAAGTGCCTG 900
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Db 901 TGACAAAGCCCTTCTCGAGAGGAGCAGCTCGCCTTACTCTGGGAGCGTCACTCTGGGCT 960
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Db 961 CGAGTACTTGACCTGACGAGAGTCTGTCACAGGACATCAAGCCATCCAACTGCTCCT 1020
QY 1021 GGGGGATGATGGGCACTGTAAGATTCGCGAATTGCGGTGAGCAACCAAGTTTGAAGGGAA 1080
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QY 1081 CGAGCTCAGCTGTCCAGCAGCGGGGAACCCAGCAATTCATGGCCCCCGAGGCCATTTC 1140
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QY 1141 TGATTCCGGCCAGAGCTTCACTGGGAAGGCTTGGATGTATGGGCCACTGGCGTCAAGTT 1200
Db 1141 TGATTCCGGCCAGAGCTTCACTGGGAAGGCTTGGATGTATGGGCCACTGGCGTCAAGTT 1200
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Db 1201 GTACTGCTTGTCTATGGGAAGTGCCCAATTCATCGACGATTTTCATCTCTGGCCCTCCACAG 1260
QY 1261 GAAGATCAAGAAATGAGCCCGTGTGTCTTGAGGAGCCAGAAATACGAGGAGAGCTCAA 1320
Db 1261 GAAGATCAAGAAATGAGCCCGTGTGTCTTGAGGAGCCAGAAATACGAGGAGAGCTCAA 1320
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QY 1381 CAAGTTGCACCCCTTGGGTGACCAAGAACGGGAGGAGCCCTCTCTTCGAGGAGGAGCA 1440
Db 1381 CAAGTTGCACCCCTTGGGTGACCAAGAACGGGAGGAGCCCTCTCTTCGAGGAGGAGCA 1440
QY 1441 CTGAGGCTGTGTGAGGTGACAGAGGGGAGGTTAAGAACTCAGTCAAGGCTCATCCCAG 1500
Db 1441 CTGAGGCTGTGTGAGGTGACAGAGGGGAGGTTAAGAACTCAGTCAAGGCTCATCCCAG 1500
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QY 1561 TGAGCCCCCAGGCGAGGGAAGAGCGATCCATGTCTGTCTCGAGGAACCTACTGTGTAA 1620
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Db 1741 CAGAGGCCACCCTCTATGCAACAGCGCCGCCAGGCGAGGGGGTGGGAGCTGCGAGCC 1800
QY 1801 CCACTCCCGCCCTCTCCCATCTGCTGTGATGACCTTCCAGCAGCAGCTCCAGGGAGCAG 1860
Db 1801 CCACTCCCGCCCTCTCCCATCTGCTGTGATGACCTTCCAGCAGCAGCTCCAGGGAGCAG 1860
QY 1861 ACTGGAATGATGTCAATTTGGGGTCTTGGGGGAGGGCTCCACAGAGCCCATCTCCTCT 1920
Db 1861 ACTGGAATGATGTCAATTTGGGGTCTTGGGGGAGGGCTCCACAGAGCCCATCTCCTCT 1920
QY 1921 TCTTGGCCCTCTCTTGGCTGACCCATTTCTGTGGGGAACCGGGTGCCTATGAGGCTCAG 1980
Db 1921 TCTTGGCCCTCTCTTGGCTGACCCATTTCTGTGGGGAACCGGGTGCCTATGAGGCTCAG 1980
QY 1981 AAATGCCACCCGCTGGTGGCATGGCTGGGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2040
Db 1981 AAATGCCACCCGCTGGTGGCATGGCTGGGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2040
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QY 2101 TGCGTCACTGCGCACAGGCAATGTGTGGAGAGGGGGGTACCTTGCACCACTTGGGGTGGT 2160
Db 2101 TGCGTCACTGCGCACAGGCAATGTGTGGAGAGGGGGGTACCTTGCACCACTTGGGGTGGT 2160
QY 2161 GGCACACAGAGCTCTTGTCTATTTCAGACGCT 2190
Db 2161 GGCACACAGAGCTCTTGTCTATTTCAGACGCT 2190

RESULT 2
US-10-690-617-1
; Sequence 1, Application US/10690617
; Publication No. US20040086926A1
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui et al.

; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE OF INVENTION: THEROPF
; FILE REFERENCE: CL000904DIV II
; CURRENT APPLICATION NUMBER: US/10/690,617
; CURRENT FILING DATE: 2003-10-23
; PRIOR APPLICATION NUMBER: 60/247,031
; PRIOR FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: 09/729,995
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2190
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-690-617-1

Query Match		100.0%	Score 2190;	DB 17;	Length 2190;
Best Local Similarity		100.0%;	Pred. No. 0;		
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DB	1	CGCCGCGGCGGCTGAGCTCGCGCATCTGGGCCCCAGCGAGGCGGTGCGGGCGGGCGGCG	60		
QY	61	GGCGGGGCGCGCAGCAGGAGCGAGTGGGGCGCGCCCGCGGCGCCACGACACTGTCGCC	120		
DB	61	GGCGGGGCGCGCAGCAGGAGCGAGTGGGGCGCGCCCGCGGCGCCACGACACTGTCGCC	120		
QY	121	GGCGCCAGGTTCACAAAGGCTACGCGAAGAAACCCCTTGACTGAGCAATGGAGGG	180		
DB	121	GGCGCCAGGTTCACAAAGGCTACGCGAAGAAACCCCTTGACTGAGCAATGGAGGG	180		
QY	181	GGGTCCAGGTCTGCTGCGAGGAGTGGTGGCGCAGAGCTGGTAGAACGGTGTGGA	240		
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QY	241	CGATGTGACTCACTTGGAGGAGCAGATGGTGGCCAGAGCCCTACTAGAAACGGTGTGGA	300		
DB	241	CGATGTGACTCACTTGGAGGAGCAGATGGTGGCCAGAGCCCTACTAGAAACGGTGTGGA	300		
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DB	301	CCCCCGACAGCGGCGCAGAGTGGTGGTGTGATCCCTGGCAGTACTTCAAGACTGTCGCC	360		
QY	361	AGCCCGGCTAGCCTCTCAGCCAGAGAGCTTTCCTACAGGAGCGGCCAGCAGGAGCTA	420		
DB	361	AGCCCGGCTAGCCTCTCAGCCAGAGAGCTTTCCTACAGGAGCGGCCAGCAGGAGCTA	420		
QY	421	TCTGGAGCGCAGGCTGGGCTTATGCCACGGGGGCTGCGAGCCACATCTCCCGCGGGC	480		
DB	421	TCTGGAGCGCAGGCTGGGCTTATGCCACGGGGGCTGCGAGCCACATCTCCCGCGGGC	480		
QY	481	CTGGCGGAGGCCACCATCGAGTCCCAACAAGTGGGCTTATGCCACGGGGGCTGCGAGCC	540		
DB	481	CTGGCGGAGGCCACCATCGAGTCCCAACAAGTGGGCTTATGCCACGGGGGCTGCGAGCC	540		
QY	541	GCAGCTGAACAGTACAGCTGACAGTGTGAGATTGGCAAGGGTGGCTACGGTGTGTGAG	600		
DB	541	GCAGCTGAACAGTACAGCTGACAGTGTGAGATTGGCAAGGGTGGCTACGGTGTGTGAG	600		
QY	601	GCTGCGCTACACGAAAGTGAAGACAGACACTATGCAATGAAAGTCTTTCACAAAAGAA	660		
DB	601	GCTGCGCTACACGAAAGTGAAGACAGACACTATGCAATGAAAGTCTTTCACAAAAGAA	660		
QY	661	GTTACTGAAGCAGTATGGCTTTCCACGTGCGCTTCCCGCAGAGGGTCCAGAGTGCCTC	720		
DB	661	GTTACTGAAGCAGTATGGCTTTCCACGTGCGCTTCCCGCAGAGGGTCCAGAGTGCCTC	720		
QY	721	GGGAGGACCGACGAGCAGTCTGCTGCGGCTGGAGCGGGTGTACCAAGGAGATTGCCATCT	780		
DB	721	GGGAGGACCGACGAGCAGTCTGCTGCGGCTGGAGCGGGTGTACCAAGGAGATTGCCATCT	780		

QY	781	GAAGAAGCTGGACCAACGTAATGTGGTCAAACTGATCGAGGTCTCTGGATGACCCAGCTGA	840
DB	781	GAAGAAGCTGGACCAACGTAATGTGGTCAAACTGATCGAGGTCTCTGGATGACCCAGCTGA	840
QY	841	GGACAACTCTATTGGTGTGGTGTGACCTCTGAGAAAGGGGCCCGTCACTGGAAGTGCCTTG	900
DB	841	GGACAACTCTATTGGTGTGGTGTGACCTCTGAGAAAGGGGCCCGTCACTGGAAGTGCCTTG	900
QY	901	TGACAAAGCCCTTCTCGGAGGAGCAAGCTCGCTTACCTTGGCGGACGTCATCTCTGGGCT	960
DB	901	TGACAAAGCCCTTCTCGGAGGAGCAAGCTCGCTTACCTTGGCGGACGTCATCTCTGGGCT	960
QY	961	CGAGTACTTGCACTGCCAGAAAGATCGTCCACAGGAGACATCAAGCCATCCAACTCTCTCT	1020
DB	961	CGAGTACTTGCACTGCCAGAAAGATCGTCCACAGGAGACATCAAGCCATCCAACTCTCTCT	1020
QY	1021	GGGGATGATGGGACGCTGAAGATCGCCGACTTTGGCGTTCAGCAACCAAGTTTGAGGGGAA	1080
DB	1021	GGGGATGATGGGACGCTGAAGATCGCCGACTTTGGCGTTCAGCAACCAAGTTTGAGGGGAA	1080
QY	1081	CGACGCTCAGCTGTCCAGCAGCGCGGAAACCCAGCATTCATGGCCCCCGAGGCCATTTC	1140
DB	1081	CGACGCTCAGCTGTCCAGCAGCGCGGAAACCCAGCATTCATGGCCCCCGAGGCCATTTC	1140
QY	1141	TGATTCGGGCCAGAGCTTTCAGTGGGAAAGCCCTTGGATGTATGGGCCACTGGCGTCACT	1200
DB	1141	TGATTCGGGCCAGAGCTTTCAGTGGGAAAGCCCTTGGATGTATGGGCCACTGGCGTCACT	1200
QY	1201	GTACTGCTTTGTCTATGGAAGTGGCCCATTCATCGAAGATTCATCTCTGGGCCCTCAG	1260
DB	1201	GTACTGCTTTGTCTATGGAAGTGGCCCATTCATCGAAGATTCATCTCTGGGCCCTCAG	1260
QY	1261	GAAGATCAAGATGAGCCGCTGCTTCTTCAGGAGCCAGAAATTCAGCGAGGAGCTCAA	1320
DB	1261	GAAGATCAAGATGAGCCGCTGCTTCTTCAGGAGCCAGAAATTCAGCGAGGAGCTCAA	1320
QY	1321	GGACCTGATCTCTGAAGATGTTAGACAAGATCCCGAGAGCAGAAATGGGGTSCCAGACAT	1380
DB	1321	GGACCTGATCTCTGAAGATGTTAGACAAGATCCCGAGAGCAGAAATGGGGTSCCAGACAT	1380
QY	1381	CAAGTGTGACCTTGGGTGACCAAGAACGGGAGAGAGCCCTTCTCTGGAGGAGGAGCA	1440
DB	1381	CAAGTGTGACCTTGGGTGACCAAGAACGGGAGAGAGCCCTTCTCTGGAGGAGGAGCA	1440
QY	1441	CTGACGCTGTGTGAGGTGACAGAGGGGAGGTTAAGAACTCAGTCAGGCTCATCCCCAG	1500
DB	1441	CTGACGCTGTGTGAGGTGACAGAGGGGAGGTTAAGAACTCAGTCAGGCTCATCCCCAG	1500
QY	1501	CTGGACCAAGGTGATCTCTGGTGAAGTCCATGCTGAGGAGGCTTCTTTGGGAAACCCGTT	1560
DB	1501	CTGGACCAAGGTGATCTCTGGTGAAGTCCATGCTGAGGAGGCTTCTTTGGGAAACCCGTT	1560
QY	1561	TGAGCCCCAGGACCGGAGGAGAGCGATTCATGTCGTCCAGGAAACCTTACTGCTGAA	1620
DB	1561	TGAGCCCCAGGACCGGAGGAGAGCGATTCATGTCGTCCAGGAAACCTTACTGCTGAA	1620
QY	1621	AGAGGGTGTGGTGAAGGGGCAAGAGCCAGAGCTCCCCGGCGTCCAGGAGAGCAGGCG	1680
DB	1621	AGAGGGTGTGGTGAAGGGGCAAGAGCCAGAGCTCCCCGGCGTCCAGGAGAGCAGGCG	1680
QY	1681	TGCATCTTGAGCCCTGATGACCCAGGGCACCCGGGACACACTCATCCCCGGCTC	1740
DB	1681	TGCATCTTGAGCCCTGATGACCCAGGGCACCCGGGACACACTCATCCCCGGCTC	1740
QY	1741	CAGAGCCCCACCTCATGCAACAGCCGCCCGGAGGAGGAGGCTGGGAGTGCAGCC	1800
DB	1741	CAGAGCCCCACCTCATGCAACAGCCGCCCGGAGGAGGAGGCTGGGAGTGCAGCC	1800
QY	1801	CCACTCCCGCCCTCCCTCCCTGCTGCTGATGACCTCCAGCAGCAGTCCAGGAGCAG	1860
DB	1801	CCACTCCCGCCCTCCCTCCCTGCTGCTGATGACCTCCAGCAGCAGTCCAGGAGCAG	1860

QY 1861 ACTGGAATGATGTCATTTGGGGCTTTGGGGGAGGGCTCCACAGAGCCATCTCTCTCT 1920
Db |||||||
QY 1861 ACTGGAATGATGTCATTTGGGGCTTTGGGGGAGGGCTCCACAGAGCCATCTCTCTCT 1920
Db |||||||
QY 1921 TCTTGGCCCTCCTTGGGCTGACCCATCTCTGTGGGAAACCGGGTGGCCATGGAGCCTCAG 1980
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QY 1981 AAATGCCACCCGGCTGGTGGCATGGCTGGGCGAGGAGCAGAGGAGAGACCAAGAT 2040
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QY 2041 GGCAGGTGGAGGCGGAGGCTTTACACACGAGGAGAGCTCCCGCTGGGGCCGGGCGAGGCC 2100
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QY 2041 GGCAGGTGGAGGCGGAGGCTTTACACACGAGGAGAGCTCCCGCTGGGGCCGGGCGAGGCC 2100
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QY 2101 TGGCTCAGCTGCCACAGGCGATATGGTGGAGAGGGGGTACCTGCCACCTTGGGGTGGT 2160
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QY 2101 TGGCTCAGCTGCCACAGGCGATATGGTGGAGAGGGGGTACCTGCCACCTTGGGGTGGT 2160
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QY 2161 GGCACACAGAGCTCTGTCTATTACAGAGCT 2190
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QY 2161 GGCACACAGAGCTCTGTCTATTACAGAGCT 2190
Db |||||||

RESULT 3

US-10-168-582-14
; Sequence 14, Application US/10168582
; Publication No. US20040058426A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: YANG, Junming
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: BURFORD, Neil
; APPLICANT: AU-YOUNG, Janice
; APPLICANT: LU, Dyung Aina M.
; APPLICANT: REDDY, Roopa
; APPLICANT: YUE, Henry
; APPLICANT: YAO, Monique G.
; APPLICANT: LAL, Preeti
; APPLICANT: KAHN, Farrah A.
; TITLE OF INVENTION: HUMAN KINASES
; FILE REFERENCE: PI-0002 PCT
; CURRENT APPLICATION NUMBER: US/10/168,582
; CURRENT FILING DATE: 2002-06-20
; PRIOR APPLICATION NUMBER: 60/172,066; 60/176,107; 60/177,731
; PRIOR FILING DATE: 1999-12-23; 2000-01-14; 2000-01-14
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PERL Program
; SEQ ID NO 14
; LENGTH: 3501
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20040058426A1 2041716CB1
US-10-168-582-14

Query Match 91.4%; Score 2001.6; DB 13; Length 3501;
Best Local Similarity 98.4%; Pred. No. 0;
Matches 2054; Conservative 0; Mismatches 4; Indels 30; Gaps 2;
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QY 190 TGTCTGTCAGGATCCTCGGCGAGAGCTGGTAGAACCGGGTGGCCCATCGATGTGAC 249
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QY 82 TGTCTGTCGACGATCCTCGGCGAGAGCTGGTAGAACCGGGTGGCCCATCGATGTGAC 141
Db |||||||
QY 250 TCATTGGAGGAGCAGATGGTGGCCGAGAGCTTACTAGAAACGGTGTGACCCCCCACC 309
Db |||||||
QY 142 TCATTGGAGGAGCAGATGGTGGCCGAGAGCTTACTAGAAACGGTGTGACCCCCCACC 201
Db |||||||

QY 310 ACGGGCAGAGCTGCCCTCTGTGATCCCTGGCAGTACTTCAAGACTGCTCCAGGCCGCC 369
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QY 202 ACGGGCAGAGCTGCCCTCTGTGATCCCTGGCAGTACTTCAAGACTGCTCCAGGCCGCC 261
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QY 370 TAGCCTCTCAGCCAGGAAGCTTTCCCTACAGGAGCGGCCAGCAGGAAGTATCTGGAGGC 429
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QY 262 TAGCCTCTCAGCCAGGAAGCTTTCCCTACAGGAGCGGCCAGCAGGAAGTATCTGGAGGC 321
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QY 430 GCAAGCTGGGCCCTTATGCCACAGGGGCTGCCAGCAGCATCTCCCCCGGCGCTGGCGGAG 489
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QY 322 GCAAGCTGGGCCCTTATGCCACAGGGGCTGCCAGCAGCATCTCCCCCGGCGCTGGCGGAG 381
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QY 490 GCCCAACATCGAGTCCCAACCACTGGCCATCTCAGATGACAGAGACTGCGTCAGACTGAA 549
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QY 382 GCCCAACATCGAGTCCCAACCACTGGCCATCTCAGATGACAGAGACTGCGTCAGACTGAA 441
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QY 550 CCAGTACAAGCTCAGAGTGAGATTGGCA-----AGGG 582
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QY 442 CCAGTACAAGCTCAGAGTGAGATTGGCAAGGTGGGGCTGACTGATGCCTATCTGCAGGG 501
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QY 583 TGCCCTACGTTGGTGGTGGCTGCCCTACAAAGAAAGTGAAGACAGACACTATGCAATGAA 642
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QY 502 TGCCTACGGTGGTGGTGGCTGCCCTACAAAGAAAGTGAAGACAGACACTATGCAATGAA 561
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QY 643 AGTCTTTCCAAAAGAAAGTTACTGAAGCAGTATGGCTTTCCAGCTGCCCTCCCGGAG 702
Db |||||||
QY 562 AGTCTTTCCAAAAGAAAGTTACTGAAGCAGTATGGCTTTCCAGCTGCCCTCCCGGAG 621
Db |||||||
QY 703 AGGTGCCAGGCTGCCAGGGAGGACAGCAAGCAGAGCTGCTGCCCTGGAGGGGTGTA 762
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QY 622 AGGTGCCAGGCTGCCAGGGAGGACAGCAAGCAGAGCTGCTGCCCTGGAGGGGTGTA 681
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QY 763 CAGAGAGATTGCCATCTCTGAAGAAGCTGAGACAGCTGAATGTGGTCAAACCTGATCGAGGT 822
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QY 682 CCAGAGATTGGCCATCTCTGAAGAAGCTGGACCACTGAATGTGGTCAAACCTGATCGAGGT 741
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QY 823 CTTGGATGACCCAGCTGAGGACAACTCTATTATTGGTGTGGCTCTCTGAGAAGGGGCC 882
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QY 742 CTTGGATGACCCAGCTGAGGACAACTCTATTATTGG---TTGACCTCTCTGAGAAGGGGCC 798
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QY 883 CGTCATGGAAGTGCCTGTGACAAAGCCCTCTCTCGAGGAGCAAGCTGCTCTACCTGCG 942
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QY 799 CGTCATGGAAGTGCCTGTGACAAAGCCCTCTCTCGAGGAGCAAGCTGCTCTACCTGCG 858
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QY 943 GAGCTCATCTCGGCTCGAGTACTTGCTACTGCGAGAAATGTCACAGGAGCAATCAA 1002
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QY 859 GAGCTCATCTCGGCTCGAGTACTTGCTACTGCGAGAAATGTCACAGGAGCAATCAA 918
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QY 1003 GCCATCCAACCTGCTCTCTGGGGGATGATGGCCACGCTGAAGATCGCCGACTTTGGCGTCAG 1062
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QY 1063 CAACCAAGTTGAGGGGAAACGACGCTCAGCTGTTCAGACGCGGGGAAACCCAGCATTCAT 1122
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QY 979 CAACCAAGTTGAGGGGAAACGACGCTCAGCTGTTCAGACGCGGGGAAACCCAGCATTCAT 1038
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QY 1123 GGGCCCGAGGCCATTTCTGATTTCCGGCCAGAGCTTCAGTGGGAAGGCTTGGATGTATG 1182
Db |||||||
QY 1039 GGGCCCGAGGCCATTTCTGATTTCCGGCCAGAGCTTCAGTGGGAAGGCTTGGATGTATG 1098
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QY 1183 GGCACATGGCGCTCACGTTGCTGCTGCTGCTATGGGAAGTGGCCCATTCATCGACGATTT 1242
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QY 1099 GGCACATGGCGCTCACGTTGCTGCTGCTGCTATGGGAAGTGGCCCATTCATCGACGATTT 1158
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QY 1243 CATCTGGCCCTCCACAGGAAGATCAAGATAGCCCGTGGTGTTCCTGAGAGGCCAGA 1302
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QY 1303 AATCAGGAGGAGCTCAAGGACCTGATCCTGGAAGATGTTAGACAAGAAATCCCGAGAGCAG 1362
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QY 1219 AATCAGGAGGAGCTCAAGGACCTGATCCTGGAAGATGTTAGACAAGAAATCCCGAGAGCAG 1278
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QY 1363 AATTGGGTGGCAGACATCAAGTTGCAACCTTGGGTGACCAAGAGCGGGAGAGCCCT 1422
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QY 1279 AATTGGGTGGCAGACATCAAGTTGCAACCTTGGGTGACCAAGAGCGGGAGAGCCCT 1338
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QY 1423 TCCTTTGGAGGAGGAGCACTGACAGCGTGTGTGAGGTGACAGAGGGGAGGTTAAGAACTC 1482
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QY 1339 TCCTTTGGAGGAGGAGCACTGACAGCGTGTGTGAGGTGACAGAGGGGAGGTTAAGAACTC 1398
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QY 1483 AGTCAGGCTATCCCGAGTGGACCAAGCGTGTATCTCTGTTGAAGTCACTGCTGAGAAAGC 1542
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QY 1399 AGTCAGGCTATCCCGAGTGGACCAAGCGTGTATCTCTGTTGAAGTCACTGCTGAGAAAGC 1458
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QY 1543 TTCTTTGGGAACCCGTTTGGAGCCCGACGACGAGGAGGAGGATCCATCTCTGCTCC 1602
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QY 1459 TTCTTTGGGAACCCGTTTGGAGCCCGACGACGAGGAGGAGGATCCATCTCTGCTCC 1518
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QY 1603 AGGAAACCTACTGTGTGAAGAGGGTGTGTGAAGGGGGGCAAGAGCCAGAGCTCCCGG 1662
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QY 1519 AGGAAACCTACTGTGTGAAGAGGGTGTGTGAAGGGGGGCAAGAGCCAGAGCTCCCGG 1578
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QY 1663 CGTCAGGAAGAGGAGGCTGCATCTGAGCCCTGATGCAACCCAGGGGCCACCCGGGAGC 1722
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QY 1579 CGTCAGGAAGAGGAGGCTGCATCTGAGCCCTGATGCAACCCAGGGGCCACCCGGGAGC 1638
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QY 1723 ACACCTATCCCGGCTCCAGAGGCCACCCCTCATGCAACAGCCGCCCGCCAGGAGC 1782
Db |||||
QY 1639 ACACCTATCCCGGCTCCAGAGGCCACCCCTCATGCAACAGCCGCCCGCCAGGAGC 1698
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QY 1783 GGGCTGGGAGCTGCAGGCCCACTCCCGGCCCTCCCGCCATCGTGTGCATGACCTCCAGC 1842
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QY 1699 GGGCTGGGAGCTGCAGGCCCACTCCCGGCCCTCCCGCCATCGTGTGCATGACCTCCAGC 1758
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QY 1843 ACGCAGCTCCAGGAGCAGATGGAATGTATGATTTGGGGTCTTGGGGGAGGAGCTCC 1902
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QY 1759 ACGCAGCTCCAGGAGCAGATGGAATGTATGATTTGGGGTCTTGGGGGAGGAGCTCC 1818
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QY 1903 ACGAGGCCATCTCTCTTTGGCCCTCTTGGCCCTGACCCATCTCTGCGGGAACCGG 1962
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QY 1819 ACGAGGCCATCTCTCTTTGGACCTCTTGGCCCTGACCCATCTCTGCGGGAACCGG 1878
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QY 1963 GTGCCCATGGAGCTCAGAAATGCCACCCGGCTGTGGCATGGCTGGGGGAGGAGCA 2022
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QY 1879 GTGCCCATGGAGCTCAGAAATGCCACCCGGCTGTGGCATGGCTGGGGGAGGAGCA 1938
Db |||||
QY 2023 GAGGAGAGACCAAGATGGCAGGTGGAGGCGAGGCTTACCAACAGGAAGAGCTCC 2082
Db |||||
QY 1939 GAGGAGAGACCAAGATGGCAGGTGGAGGCGAGGCTTACCAACAGGAAGAGCTCC 1998
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QY 2083 GCTGGGGCGGGGAGGCGCTGCTGAGCTGACAGGCGCATATGTTGGAGAGGGGGTACC 2142
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QY 1999 GCTGGGGCGGGGAGGCGCTGCTGAGCTGACAGGCGCATATGTTGGAGAGGGGGTACC 2058
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QY 2143 TGCCCCACCTTGGGGTGGTGCCACCAAGAGCTCTTGTCTATTTCAGAGCGT 2190
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RESULT 4
US-10-333-314-39
; Sequence 39, Application US/10333314
; Publication No. US20030211093A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.; YUE, Henry
; APPLICANT: KHAN, Farrah A.; GURURAJAN, Rajagopal
; APPLICANT: HAFALIA, April J.A.; CHAWLA, Narinder K.
; APPLICANT: ARVIZU, Chandra S.; RAMKUMAR, Javalaxmi
; APPLICANT: GANDHI, Ameena R.; POLICKY, Jennifer L.
; APPLICANT: BAUGHN, Mariah R.; TRIBOULEY, Catherine M.
; APPLICANT: THORNTON, Daniel B.; BANDMAN, Olga
; APPLICANT: NGUYEN, Dannel B.; LU, Yan
; APPLICANT: BURFORD, Neil; LAU, Preeti G.
; APPLICANT: DING, Li; YAO, Monique G.
; APPLICANT: ELLIOTT, Vicki S.; RECIPON, Shirley A.
```

```
; APPLICANT: KEARNEY, Liam; LU, Dyung Aina M.
; APPLICANT: GREENWALD, Sara R.; TANG, Y. Tom
; APPLICANT: XU, Yuming; WALSH, Roderick T.
; APPLICANT: GIETZEN, Kimberly J.; YANG, Junming
; APPLICANT: JACKSON, Jennifer L.
; TITLE OF INVENTION: HUMAN KINASES
; FILE REFERENCE: PI-0162 USN
; CURRENT APPLICATION NUMBER: US/10/333,314
; CURRENT FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: PCT/US01/23092
; PRIOR FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/220,038
; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: US 60/222,112
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/222,831
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: US 60/224,729
; PRIOR FILING DATE: 2000-08-11
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PERL Program
; SEQ ID NO 39
; LENGTH: 1937
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 2190612CB1
US-10-333-314-39
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Query Match 87.1%; Score 1906.4; DB 13; Length 1937;

Best Local Similarity 99.7%; Pred. No. 0;

Matches 1910; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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QY 190 TGTCTGTCTCCAGGATCTCGGGCAGAGCTGCTGTAAGACGGGTGGCAGGCATCGATGTGAC 249
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QY 82 TGTCTGTCTCCAGGATCTCGGGCAGAGCTGCTGTAAGACGGGTGGCAGGCATCGATGTGAC 141
Db |||||
QY 250 TCACCTGGAGGAGGAGATGTTGGCCAGAGCTTACTAGAAACGGTGTGGACCCCGCCACC 309
Db |||||
QY 142 TCACCTGGAGGAGGAGATGTTGGCCAGAGCTTACTAGAAACGGTGTGGACCCCGCCACC 201
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QY 310 ACGGCCAGAGCTGCTCTGTGATCCCTGGCAGTACTTCAAGACTGCTCCAGAGCCCGGCC 369
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QY 202 ACGGCCAGAGCTGCTCTGTGATCCCTGGCAGTACTTCAAGACTGCTCCAGAGCCCGGCC 261
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QY 370 TAGCCTCTCAGCCAGGAAGCTTTCCCTACAGAGCGGCCAGCAGGAAGCTATCTGGAGGC 429
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QY 262 TAGCCTCTCAGCCAGGAAGCTTTCCCTACAGAGCGGCCAGCAGGAAGCTATCTGGAGGC 321
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QY 430 GCAGGCTGGGCTTATGCCACGGGGCTGCCAGCACAATCTCCCGCCGGGCTGGCGGAG 489
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QY 322 GCAGGCTGGGCTTATGCCACGGGGCTGCCAGCACAATCTCCCGCCGGGCTGGCGGAG 381
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QY 490 GCCCACCATCGAGTCCCAACACGTTGCCATCTCAGATGCGCAGGAGCTCGTGCGAGCTGAA 549
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QY 382 GCCCACCATCGAGTCCCAACACGTTGCCATCTCAGATGCGCAGGAGCTCGTGCGAGCTGAA 441
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QY 610 CAACGAAGTGAACAGACAGACTATGCAATGAAGTCTCTTCCAAAAGAAAGTACTGAA 669
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QY 368 CCTAGCCTCTCAGCCAGGAAGCTTTCCCTACAGGAGGGCCAGCAGGAAGCTATCTGGAG 427
DB 393 CCTAGCCTCTCAGCCAGGAAGCTTTCCCTACAGGAGGGCCAGCAGGAAGCTATCTGGAG 452
QY 428 GGCAGGCTGGGCTTTATGCGACGGGGCTTCCAGACCATCTCCCGGGGCTGGCGG 487
DB 453 GGCAGGCTGGGCTTTATGCGACGGGGCTTCCAGACCATCTCCCGGGGCTGGCGG 512
QY 488 AGGCCACCATCGAGTCCACCAACGCTGGCCATCTCAGATGCGAGGACTGCGTGCAGCTG 547
DB 513 AGGCCACCATCGAGTCCACCAACGCTGGCCATCTCAGATGCGAGGACTGCGTGCAGCTG 572
QY 548 AACCACTAAGCTGCGAGATGAGATTGCGAGGGTGCCTACGCTGTGTGAGGCTGGCC 607
DB 573 AACCACTAAGCTGCGAGATGAGATTGCGAGGGTGCCTACGCTGTGTGAGGCTGGCC 632
QY 608 TACAAACGAAGTGAAGACAGACACTATGCAATGAAAGTCTTTCCAAAAGAGTTACTG 667
DB 633 TACAAACGAAGTGAAGACAGACACTATGCAATGAAAGTCTTTCCAAAAGAGTTACTG 692
QY 668 AAGCAGTATGGCTTTCCAGCTGCGCCCTCCCGAGAGGGTCCAGGCTGCCAGGGAGGA 727
DB 693 AAGCAGTATGGCTTTCCAGCTGCGCCCTCCCGAGAGGGTCCAGGCTGCCAGGGAGGA 752
QY 728 CCAGCCAGCAGCTGCTGCGCCCTGAGCGGGTGTACAGGAGATTGCCATCTGGAAGAAG 787
DB 753 CCAGCCAGCAGCTGCTGCGCCCTGAGCGGGTGTACAGGAGATTGCCATCTGGAAGAAG 812
QY 788 CTGGACCAAGCTGAATGTGGTCAAACTGATCGAGGCTCTGATGACCCAGCTCAGAGCAAC 847
DB 813 CTGGACCAAGCTGAATGTGGTCAAACTGATCGAGGCTCTGATGACCCAGCTCAGAGCAAC 872
QY 848 CTCTATTTGGTGTGAACTCTCTGAGAAAGGGCCCGTCAATGAAAGTGCCCTGTGACAA 907
DB 873 CTCTATTTGGTGTGAACTCTCTGAGAAAGGGCCCGTCAATGAAAGTGCCCTGTGACAA 932
QY 908 CCTTCTCGGAGGAGCAAGCTGCTCTACCTGCGGAGCTCATCTGGGGCTCGAGTAC 967
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QY 968 TTGCACTGCCAAGATCGTCCACAGGGACATCAAGCCATCAACCTGCTCTGGGGAT 1027
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QY 1028 GATGGGCAAGTATCGGCACTTTGGCGTACGCAACCAAGTTTGGGGGCAACGACGT 1087
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DB 1293 AAGATGAGCCGCTGGTGTCTCTGAGGAGCCAGAAATCAGGAGGAGCTCAAGACCTG 1352
QY 1328 ATCTCTGAAGATGTTAGACAAAGATCCGAGACGAGAAATGGGGTCCAGACATCAAGTTG 1387
DB 1353 ATCTCTGAAGATGTTAGACAAAGATCCGAGACGAGAAATGGGGTCCAGACATCAAGTTG 1412
QY 1388 CACCTCTGGGTGACCAAGACGGGAGGAGCCCTTCTCTGGAGGAGGAGCACTGCAGC 1447
DB 1413 CACCTCTGGGTGACCAAGACGGGAGGAGCCCTTCTCTGGAGGAGGAGCACTGCAGC 1472

QY 1448 GTGGTGGAGTGAACAGAGGGGAGGTTAAGAACTCAGTCAGGCTCATCCCAGCTGGACC 1507
DB 1473 GTGGTGGAGTGAACAGAGGGGAGGTTAAGAACTCAGTCAGGCTCATCCCAGCTGGACC 1532
QY 1508 ACGETGATCTCGTGAAGTCCATGCTGAGGAAGCGTTCTTTGGGAAACCGTTTGAGCCC 1567
DB 1533 ACGETGATCTCGTGAAGTCCATGCTGAGGAAGCGTTCTTTGGGAAACCGTTTGAGCCC 1592
QY 1568 CAGGACCGAGGAGGAGCGATCCATGCTCTCCAGGAAACCTACTGCTGGAAGAGGG 1627
DB 1593 CAAGCACGAGGAGGAGCGATCCATGCTCTCCAGGAAACCTACTGCTGGAAGAGGG 1652
QY 1628 TTTGTGAAGGGGCGGAGAGCCAGAGCTCCCGGCGTCCAGGAAGACGA 1677
DB 1653 TTTGTGAAGGGGCGGAGAGCCAGAGCTCCCGGCGTCCAGGCTTACCA 1702

RESULT 6

US-10-391-364-41
; Sequence 41, Application US/10391364
; Publication No. US20040121349A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Meyers, Rachel E.
; APPLICANT: Carroll, Joseph M.
; APPLICANT: Cook, William James
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: Welch, Nadine S.
; APPLICANT: Bandaru, Rajasekhar
; TITLE OF INVENTION: NOVEL 27877, 18080, 14081, 32140, 50352,
; TITLE OF INVENTION: 16658, 14223, 16002, 50566, 65552 AND 65577 MOLECULES AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: MP103-0190NM1
; CURRENT APPLICATION NUMBER: US/10/391,364
; PRIOR FILING DATE: 2003-03-18
; PRIOR APPLICATION NUMBER: US 09/950,370
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: US 60/231,084
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: US 10/294,039
; PRIOR FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 60/338,587
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 10/266,035
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: US 60/328,198
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: US 09/717,926
; PRIOR FILING DATE: 2000-11-21
; PRIOR APPLICATION NUMBER: US 60/214,707
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: US 10/268,036
; PRIOR FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US 60/327,820
; PRIOR FILING DATE: 2001-10-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 41
; LENGTH: 2711
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (198)...(1883)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(2711)
; OTHER INFORMATION: n = A,T,C or G
US-10-391-364-41

Query Match 74.7%; Score 1636.2; DB 17; Length 2711;
Best Local Similarity 98.9%; Pred. No. 0;

Matches 1652; Conservative 4; Mismatches 13; Indels 1; Gaps 1;			
QY	8	GGGCTGAGCTCGCGATCTGGGCCCCAGAGCGGTGGGCGGGCGGGCGGG	67
Db	34	GGGCTGNGCTCSRCGWTYCCGGTCCCGCCAGCAGCGGTGGGCGGGCGGGCGGG	93
QY	68	GCSCGACAGAGAGCGAGTGGGCGCCCGCCCGGSCCAGCAGCACTGTGCGCCGGCGCC	127
Db	94	GCSCGACAGAGCGAGCGAGTGGGCGG--CCGCCGGCGCGCGACACTGTGCCCGGGCGCC	152
QY	128	AGGTTCCTCAACAGGCTTACCGAGAGAACCCCTTGACTGAAGCAATGGAGGGGGTCCA	187
Db	153	AGGTTCCTCAACAGGCTTACCGAGAGAACCCCTTGACTGAAGCAATGGAGGGGGTCCA	212
QY	188	GCTGTCTGCTGCCAGGATCTCGGGCAGAGCTGGTAGAACGGGTGGCAGCCATCGATGTG	247
Db	213	GCTGTCTGCTGCCAGGATCTCGGGCAGAGCTGGTAGAACGGGTGGCAGCCATCGATGTG	272
QY	248	ACTCACTTGAGAGGCGAGTGGGCCAGAGCCTACTAGAACGGGTGGACCCGCCA	307
Db	273	ACTCACTTGAGAGGCGAGTGGGCCAGAGCCTACTAGAACGGGTGGACCCGCCA	332
QY	308	CCACGGGCCAGAGCTGCTCTGTGATCCCTGGCAGTACTTCAAGACTGCTCCAGCCCGG	367
Db	333	CCACGGGCCAGAGCTGCTCTGTGATCCCTGGCAGTACTTCAAGACTGCTCCAGCCCGG	392
QY	368	CCTAGCCTCTCAGCAGAGAGCTTTCCTCAGAGCGGCCAGAGAGAGCTATCTGGAG	427
Db	393	CCTAGCCTCTCAGCAGAGAGCTTTCCTCAGAGCGGCCAGAGAGAGCTATCTGGAG	452
QY	428	GGCAGAGCTGGGCTTATGCCACGGGCGCTGCCAGCCACATCTCCCCGGGCGCTGCGG	487
Db	453	GGCAGAGCTGGGCTTATGCCACGGGCGCTGCCAGCCACATCTCCCCGGGCGCTGCGG	512
QY	488	AGGCCACCACTCGAGTCCACCACTGGCCATCTCAGATGACAGAGACTGCGTGCAGCTG	547
Db	513	AGGCCACCACTCGAGTCCACCACTGGCCATCTCAGATGACAGAGACTGCGTGCAGCTG	572
QY	548	AACCACTGACAGCTGACAGATGGGCMAGGGTGCCTACGGTGTGGTAGGCTGGCC	607
Db	573	AACCACTGACAGCTGACAGATGGGCMAGGGTGCCTACGGTGTGGTAGGCTGGCC	632
QY	608	TACAAACGAAGTGAAGCAGACACTATGCAATGAAGTCTTTCCTCAAAAGAACTTACTG	667
Db	633	TACAAACGAAGTGAAGCAGACACTATGCAATGAAGTCTTTCCTCAAAAGAACTTACTG	692
QY	668	AAGCAGTATGGCTTTCCACGTGCGCCCTCCCCGAGAGGGTCCCAAGGTGCCAGGGAGA	727
Db	693	AAGCAGTATGGCTTTCCACGTGCGCCCTCCCCGAGAGGGTCCCAAGGTGCCAGGGAGA	752
QY	728	CCAGCCAGCAGCTGCTGCCCTGGAGCGGGGTACCAAGAGATGCCATCTGAAGAG	787
Db	753	CCAGCCAGCAGCTGCTGCCCTGGAGCGGGGTACCAAGAGATGCCATCTGAAGAG	812
QY	788	CTGACCAACGTAATGTGTCCTCAACTGATCGAGTCTCTGGATGACCCAGCTGAGACAAC	847
Db	813	CTGACCAACGTAATGTGTCCTCAACTGATCGAGTCTCTGGATGACCCAGCTGAGACAAC	872
QY	848	CTCTATTGGTGTGTTGACCTCTGAGAAAGGGGCCGCTCATGGAAGTGCCTGTGACAAG	907
Db	873	CTCTATTGGTGTGTTGACCTCTGAGAAAGGGGCCGCTCATGGAAGTGCCTGTGACAAG	932
QY	908	CCCTTCTCGGAGGACAGCTCGCTCTACCTCGGGGACGTCATCTGGGCTCGAGTAC	967
Db	933	CCCTTCTCGGAGGACAGCTCGCTCTACCTCGGGGACGTCATCTGGGCTCGAGTAC	992
QY	968	TTGCACTCCAGAAAGTCTGTCACAGGACATCAAGCCATCCAACTCTCTCTGGGGAT	1027
Db	993	TTGCACTCCAGAAAGTCTGTCACAGGACATCAAGCCATCCAACTCTCTCTGGGGAT	1052
QY	1028	GATGGGACGTGAAGATCGCCGACTTTGGCGTCAAGAACAGTGTGGGGGAAACGACCT	1087
Db	1053	GATGGGACGTGAAGATCGCCGACTTTGGCGTCAAGAACAGTGTGGGGGAAACGACCT	1112

QY	1088	CAGCTCTCAGCACGGCGGAACCCAGACATTCATGGCCCCCGAGGCCATTTCTGATTCC	1147
Db	1113	CAGCTCTCAGCACGGCGGAACCCAGACATTCATGGCCCCCGAGGCCATTTCTGATTCC	1172
QY	1148	GGCCAGAGCTTCAGTGGGAGGCGCTTGGATGTATGGGCCACTGGCGCTCAGTTGTACTGC	1207
Db	1173	GGCCAGAGCTTCAGTGGGAGGCGCTTGGATGTATGGGCCACTGGCGCTCAGTTGTACTGC	1232
QY	1208	TTTGTCTATGGGAAGTGCCTCATTCAGCAGATTTTCTGCGCCCTCCACAGGAAGATC	1267
Db	1233	TTTGTCTATGGGAAGTGCCTCATTCAGCAGATTTTCTGCGCCCTCCACAGGAAGATC	1292
QY	1268	ARGAATGAGCCCTGGTGTCTTCTGAGGAGCCAGAAATCAGCCAGGAGCTCAAGGACCTG	1327
Db	1293	ARGAATGAGCCCTGGTGTCTTCTGAGGAGCCAGAAATCAGCCAGGAGCTCAAGGACCTG	1352
QY	1328	ATCCTGAAGATGTTAGACAGAAATCCCGAGACAGAAATTTGGGTGCCAGACATCAAGTTG	1387
Db	1353	ATCCTGAAGATGTTAGACAGAAATCCCGAGACAGAAATTTGGGTGCCAGACATCAAGTTG	1412
QY	1388	CACCTTTGGTGAACAGAAACGGGAGGAGCCCTTCTTCCGAGGAGGAGCACTGCAGC	1447
Db	1413	CACCTTTGGTGAACAGAAACGGGAGGAGCCCTTCTTCCGAGGAGGAGCACTGCAGC	1472
QY	1448	GTGCTGAGGTGACAGAGGGGGAGGTTAAGAACTCAGTCAGGCTCATCCCGAGCTGGACC	1507
Db	1473	GTGCTGAGGTGACAGAGGGGGAGGTTAAGAACTCAGTCAGGCTCATCCCGAGCTGGACC	1532
QY	1508	ACGCTGATCTCGTGAAGTCCATGCTGAGGAAGCGTTCTTTGGGAACCCGTTTGAGCCC	1567
Db	1533	ACGCTGATCTCGTGAAGTCCATGCTGAGGAAGCGTTCTTTGGGAACCCGTTTGAGCCC	1592
QY	1568	CAGCAGGAGGAGAGGCGATCCATGCTCTGCTCCAGGAACCTTACTGTGGAAGAGGG	1627
Db	1593	CAAGCAGGAGGAGAGGCGATCCATGCTCTGCTCCAGGAACCTTACTGTGGAAGAGGG	1652
QY	1628	TTTGGTGAAGGGGCAAGAGCCAGAGCTCCCGGGCGTCCAGGAAGACGA	1677
Db	1653	TTTGGTGAAGGGGCAAGAGCCAGAGCTCCCGGGCGTCCAGGAAGACGA	1702

RESULT 7

US-10-302-172-433
; Sequence 433, Application US/10302172
; Publication No. US20040053250A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Xue, Aidong J.
; TITLE OF INVENTION: No. US20040053250A1el Arginine-rich Protein-like Nucleic Acids a
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 803_1CNCP
; CURRENT APPLICATION NUMBER: US/10/302,172
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/225,251
; PRIOR FILING DATE: 2002-08-20
; PRIOR APPLICATION NUMBER: PCT US02/05095
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 09/799,451
; PRIOR FILING DATE: 2001-03-05
; NUMBER OF SEQ ID NOS: 950
; SOFTWARE: pt FL_genes Version 2.0
; SEQ ID NO 433_
; LENGTH: 2018
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1746)
US-10-302-172-433

Query Match

73.5%; Score 1610.2; DB 13; Length 2018;


```

; APPLICANT: Leite, Mario W.
; APPLICANT: Zhong, Haihong
; APPLICANT: Alsbrook, John P.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Burgess, Catherine E.
; TITLE OF INVENTION: No. US20040043382A1el Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-290C
; CURRENT APPLICATION NUMBER: US/10/092,900A
; CURRENT FILING DATE: 2002-03-07
; PRIOR APPLICATION NUMBER: USN 60/274,322
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: USN 60/283,675
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: USN 60/338,092
; PRIOR FILING DATE: 2001-12-03
; PRIOR APPLICATION NUMBER: USN 60/274,281
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: USN 60/274,191
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: USN 60/325,681
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: USN 60/304,354
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: USN 60/279,995
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: USN 60/294,899
; PRIOR FILING DATE: 2001-05-31
; PRIOR APPLICATION NUMBER: USN 60/287,424
; PRIOR FILING DATE: 2001-04-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 769
; SEQ ID NO 55
; LENGTH: 1611
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (52) .. (1567)
US-10-092-900A-55

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Query Match	73.1%	Score 1601.4;	DB 13;	Length 1611;
Best Local Similarity	99.6%;	Pred. No. 0;		
Matches 1605; Conservative	0;	Mismatches	6;	Indels 0; Gaps 0

QY	122	GGGCCCAAGTGTCCCAACAAAGGCTACGCAAGAAACCCCTTGTACTGAAGCAATGAGGGG	181
DB	1	GGGCCCAAGTGTCCCAACAAAGGCTACGCAAGAAACCCCTTGTACTGAAGCAATGAGGGG	60
QY	182	GGTCCAGCTGTCTGTCGCCAGGATCCTCGGCCAGAGCTGGTGAAGCGGTGCAGCCATC	241
DB	61	GGTCCAGCTGTCTGTCGCCAGGATCCTCGGCCAGAGCTGGTGAAGCGGTGCAGCCATC	120
QY	242	GATGTGACTCACTTGGAGGAGCAGATGGTGCCCAAGAGCCCTPACTAGAAAACGGTGTGGAC	301
DB	121	GATGTGACTCACTTGGAGGAGCAGATGGTGCCCAAGAGCCCTPACTAGAAAACGGTGTGGAC	180
QY	302	CCCCACCAACCGGGCCAGAGCTGCCTCTGTGATCTCTGGCAGTACTTCAAGACTGTCTCCA	361
DB	181	CCCCACCAACCGGGCCAGAGCTGCCTCTGTGATCTCTGGCAGTACTTCAAGACTGTCTCCA	240
QY	362	GCCGGGCTAGCCTCTACGACAGGAAGCTTTCCCTACAGGAGCGGCCACGAGGAGCTAT	421
DB	241	GCCGGGCTAGCCTCTACGACAGGAAGCTTTCCCTACAGGAGCGGCCACGAGGAGCTAT	300
QY	422	CTGGAGGGCGAGGCTGGGCGCTTATGCCACGGGGCCTGCCAGCCACATCTCCCCCGGGCC	481
DB	301	CTGGAGGGCGAGGCTGGGCGCTTATGCCACGGGGCCTGCCAGCCACATCTCCCCCGGGCC	360
QY	482	TGGCGGAGCCCAACCATCGAGTCCCAACACGCTGGGCCATCTCAGATGCAGAGACTGCGTG	541
DB	361	TGGCGGAGGCCCAACCATCGAGTCCCAACACGCTGGGCCATCTCAGATGCAGAGACTGCGTG	420


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Db 1501 GAAGGGTTTGGTGAAGGGGCAAGAGCCAGAGCTCCCGGGCTCCAGGAAGACGAGGCT 1560
QY 1682 GCATCTGAGCCCTCATGCACCCAGGGGCCACCCGGGAGCAGCAGCAGCATCATCC 1732
Db 1561 GCATCTGAGCCCTCATGCACCCAGGGGCCACCCGGGAGCAGCAGCAGCATCATCC 1611
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RESULT 9

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US-10-092-900A-53
; Sequence 53, Application US/10092900A
; Publication No. US20040043382A1
; GENERAL INFORMATION:
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Taupier Jr., Raymond J.
; APPLICANT: Pena, Carol E.A.
; APPLICANT: Li, Li
; APPLICANT: Zernhusen, Bryan D.
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Ji, Weizhen
; APPLICANT: Gorman, Linda
; APPLICANT: Miller, Charles E.
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Patturajan, Meera
; APPLICANT: Gangolli, Esha A.
; APPLICANT: Vernet, Corine A.M.
; APPLICANT: Guo, Xiaojia Sasha
; APPLICANT: Tchernev, Velizar T.
; APPLICANT: Fernandes, Elma R.
; APPLICANT: Casman, Stacie J.
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Liu, Yi
; APPLICANT: Anderson, David W.
; APPLICANT: Spaderna, Steven K.
; APPLICANT: Catterton, Elina
; APPLICANT: Leite, Mario W.
; APPLICANT: Zhong, Hailong
; APPLICANT: Alsbrook, John P.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Burgess, Catherine E.
; TITLE OF INVENTION: No. US20040043382A1el Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-290C
; CURRENT APPLICATION NUMBER: US/10/092,900A
; PRIOR FILING DATE: 2002-03-07
; PRIOR APPLICATION NUMBER: USSN 60/274,322
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: USSN 60/283,675
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: USSN 60/338,092
; PRIOR FILING DATE: 2001-12-03
; PRIOR APPLICATION NUMBER: USSN 60/274,281
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: USSN 60/274,191
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: USSN 60/325,681
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: USSN 60/304,354
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: USSN 60/279,995
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: USSN 60/294,899
; PRIOR FILING DATE: 2001-05-31
; PRIOR APPLICATION NUMBER: USSN 60/287,424
; PRIOR FILING DATE: 2001-04-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 768
; SEQ ID NO 53
; LENGTH: 1547
; TYPE: DNA
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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (20)..(1529)
US-10-092-900A-53
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Query Match 68.2%; Score 1493.8; DB 13; Length 1547;

Best Local Similarity 98.5%; Pred. No. 0;

Matches 1530; Conservative 0; Mismatches 17; Indels 6; Gaps 2;

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QY 154 AACCCCTTGACTGAAGCAATGAGGGGGTTCAGCTGTCTGCTGCCAGATCTCTGGGC 213
Db 1 AACCCCTTTGACTGAAGCAATGAGGGGGTTCAGCTGTCTGCTGCCAGATCTCTGGGC 60
QY 214 AGAGCTGGTAGAAACGGGTGGCAGCCATCGATGTGACTCACTTGGAGAGGAGAGATGGTGG 273
Db 61 AGAGCTGGTAGAAACGGGTGGCAGCCATCGATGTGACTCACTTGGAGAGGAGAGATGGTGG 120
QY 274 CCCAGAGCCTACTAGAAACGGTGTGGACCCGCCACCCAGCGGGCCAGAGCTGCCTCTGTGAT 333
Db 121 CCAGAGCCTACTAGAAACGGTGTGGACCCGCCACCCAGCGGGCCAGAGCTGCCTCTGTGAT 180
QY 334 CCCTGGCAGTACTTCAAGACTGCTCCAGCCGGCTAGCCTCTCAGCCAGGAAGTTTC 393
Db 181 CCCTGGCAGTACTTCAAGACTGCTCCAGCCGGCTAGCCTCTCAGCCAGGAAGTTTC 240
QY 394 CCTACAGGAGCGGCGCAGCAGGAAGCTATCTGAGGCGCAGAGGCTGGGCCCTTATGCCACGGG 453
Db 241 CTTACAGGAGCGGCGCAGCAGGAAGCTATCTGAGGCGCAGAGGCTGGGCCCTTATGCCACGGG 300
QY 454 GCCTGCCAGCCACATCTCCCGCGGCTGGCGGAGGCCACCATCGAGTCCACACCGT 513
Db 301 GCCTGCCAGCCACATCTCCCGCGGCTGGCGGAGGCCACCATCGAGTCCACACCGT 360
QY 514 GGCATCTCAGNTGAGAGGACTGCTGAGCTGAACAGTACAGTACAGCTGCAGTGAAT 573
Db 361 GGCATCTCAGNTGAGAGGACTGCTGAGCTGAACAGTACAGTACAGTGCAGTGAAT 420
QY 574 TGGCAAGGTGCTTACGGTGTGGTGGCTGCCCTACACGAAAGTGAAGAGCAGACACTA 633
Db 421 TGGCAAGGTGCTTACGGTGTGGTGGCTGCCCTACACGAAAGTGAAGAGCAGACACTA 480
QY 634 TGCATGAAGTCTTTTCCAAAAGAGTTACTGAAGCAGTATGGCTTTCCAGCTGCCGC 693
Db 481 TGCATGAAGTCTTTTCCAAAAGAGTTACTGAAGCAGTATGGCTTTCCAGCTGCCGC 540
QY 694 TCCCGCGAGAGGCTCCAGGCTGCCAGGGAGGACAGCCAGCAGAGCTGCTGCCCTGGA 753
Db 541 TCCCGCGAGAGGCTCCAGGCTGCCAGGGAGGACAGCCAGCAGAGCTGCTGCCCTGGA 600
QY 754 GCGGTGTACAGGAGATTGCCATCTCAAGAAAGCTGGACACAGTGAATGTGCTCAAACT 813
Db 601 GCGGTGTACAGGAGATTGCCATCTCAAGAAAGCTGGACACAGTGAATGTGCTCAAACT 660
QY 814 GATCAGGTCTGGATGACCCAGTGAAGCAACCTCTATTGGTGTGTTGACCTCTCTGAG 873
Db 661 GATCAGGTCTGGATGACCCAGTGAAGCAACCTCTATTGGTGTGTTGACCTCTCTGAG 717
QY 874 AAAGGGCCCTCATGGAAGTGCCTGTGACAGCCCTTCTCGAGGAGCAGAGCTCGCT 933
Db 718 CCAAGGGCCCTCATGGAAGTGCCTGTGACAGCCCTTCTCGAGGAGCAGAGCTCGCT 777
QY 934 CTACCTGCGGAGCGTCACTCTGGGGCTCGAGTACTTTCAGTGCACAGAGATGCTCCACAG 993
Db 778 CTACCTGCGGAGCGTCACTCTGGGGCTCGAGTACTTTCAGTGCACAGAGATGCTCCACAG 837
QY 994 GGAATCAAGCCATCCAACTGCTCTGGGGGATGATGGGACAGTGAAGATGCGGACTT 1053
Db 838 GGACATCAAGCCATCCAACTGCTCTGGGGGATGATGGGACAGTGAAGATGCGGACTT 897
QY 1054 TGGCGTCAGCAACCAAGTTTGAAGGGAGCAGCTCAGCTGTCCAGCAGCGGGGAGACCCC 1113
Db 898 TGGCGTCAGCAACCAAGTTTGAAGGGAGCAGCTCAGCTGTCCAGCAGCGGGGAGACCCC 957
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QY	1173	AGCATTT	CATGGCCCCCGAGGCCAATTTCTGATTC	CCGCGCCAGAGCTTCAGTGGGAAGCCCTT	1173	
Db	958	AGCATTT	CATGGCCCCCGAGGCCAATTTCTGATTC	CCGCGCCAGAGCTTCAGTGGGAAG---TTT	1014	
QY	1174	GGATG	TATGGCCCACTGGCCGTCA	CGTTGTACTGCTTTGCTATATGGGAAGTCCCATTCAT	1233	
Db	1015	GGATG	TATGGCCCACTGGCCGTCA	CGTTGTACTGCTTTGCTATATGGGAAGTCCCATTCAT	1074	
QY	1234	CGACG	ATTTCAATCCTGTGGCCCTCCACAGGAAGATCA	GAATGAGCCCGTGTGTTCCTGA	1293	
Db	1075	CGACG	ATTTCAATCCTGTGGCCCTCCACAGGAAGATCA	GAATGAGCCCGTGTGTTCCTGA	1134	
QY	1294	GGAGCC	AGAAATCAGCGAGAGAGCTCAAGGACCTGATCT	CTGAAGATGTTACACAAGATCC	1353	
Db	1135	GGAGCC	AGAAATCAGCGAGAGAGCTCAAGGACCTGATCT	CTGAAGATGTTACACAAGATCC	1194	
QY	1354	CGAGAC	GAGAAATTTGGGGTGC	CAGACATCAAGTTTGACCCCTTTGGGTGACCAAGAAGCGGGGA	1413	
Db	1195	CGAGAC	GAGAAATTTGGGGTGC	COAGNATCAAGTTTGACCCCTTTGGGTGACCAAGAAGCGGGGA	1254	
QY	1414	GGAGCC	CCCTTCCTTCGGAGGAGGACGACTCGACGGTGGT	CGAGGTGACAGAGGGGGAGGT	1473	
Db	1255	GGAGCC	CCCTTCCTTCGGAGGAGGAGCACTCGACGGTGGT	CGAGGTGACAGAGGGGGAGGT	1314	
QY	1474	TAAGAA	CTCAGTCAAGGCTCATATCCCACTCGA	CCA	CGGTGATCCTGTGTGAAGTCCATGCT	1533
Db	1315	TAAGAA	CTCAGTCAAGGCTCATATCCCACTCGA	CCA	CGGTGATCCTGTGTGAAGTCCATGCT	1374
QY	1534	GAGGAAG	CGGTTCCTTTTGGGAACCGTTTGAGCCCCAGGCGACGGAGGAACAGACGATCCAT			1593
Db	1375	GAGGAAG	CGGTTCCTTTTGGGAACCGCGTTTGAGCCCCAGGCGACGGAGGAACAGACGATCCAT			1434
QY	1594	GTCTGT	CTCCAGGAACCTACTGTGTGAAGAAGGGTTTGGTGAAGGGGGGCAAGAGCCACAGA			1653
Db	1435	GTCTGT	CTCCAGGAACCTACTGTGTGAAGAAGGGTTTGGTGAAGGGGGGCAAGAGCCACAGA			1494
QY	1654	GCTCCCC	GGGGTCCAGGAAGACGAGGCTGATCCTGTAGCCCTCGATCGACCC			1706
Db	1495	GCTCCCC	GGGGTCCAGGAAGACGAGGCTGATCCTGTAGCCCTCGATCGACCC			1547

RESULT 10

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US-09-922-138-9
; Sequence 9, Application US/09922138
; Patent No. US20020061574A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Meyers, Rachel
; APPLICANT: Silos-Santiago, Inmaculada
; TITLE OF INVENTION: 16558, 14223, AND 16002. NOVEL HUMAN
; TITLE OF INVENTION: KINASES AND USES THEREFOR
; FILE REFERENCE: 38155-20030.00
; CURRENT APPLICATION NUMBER: US/09/922,138
; CURRENT FILING DATE: 2001-11-28
; PRIOR APPLICATION NUMBER: US 60/229,299
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 1683
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-922-138-9

```

233	Qy	GAAGCCATCGATGTGACTCACCTTGGAGGAGGCGATGTTGGCCCGCAGAGCCTTACTGAAC	292
61	Db	GCAGCCATCGATGTGACTCACCTTGGAGGAGGAGGATGTTGGCCCGCAGAGCCTTACTGAAC	120
293	Qy	GGTGTGACCCCCCAACCGGGCCAGAGCTGCTCTGTGATCCCTGGCAGTACTTCAAGA	352
121	Db	GGTGTGGAACCCCAACCGGGCCAGAGCTGCTCTGTGATCCCTGGCAGTACTTCAAGA	180
353	Qy	CTGCTCCCAAGCCGGCTTAGCCTCTCAGCCAGGAAGCTTTCCTACAGAGGGCCAGCA	412
181	Db	CTGCTCCCAAGCCGGCTTAGCCTCTCAGCCAGGAAGCTTTCCTACAGAGGGCCAGCA	240
413	Qy	GGAGCTATCTGGAGCGCAGAGCTGGCCCTTATGCCACGGGGCTGCCACGCCACTCTCC	472
241	Db	GGAGCTATCTGGAGCGCAGAGCTGGCCCTTATGCCACGGGGCTGCCACGCCACTCTCC	300
473	Qy	CCCCGGGCTGGCGAGGGCCCACTATGAGTGTCCACAGCTGGCCACTCTCAGATGCAGAG	532
301	Db	CCCCGGGCTGGCGAGGGCCCACTATGAGTGTCCACAGCTGGCCACTCTCAGATGCAGAG	360
533	Qy	GACTGGTGAGCTGAAACAGTATCAAGCTGCAGAGTGAGATTGGCAAGGGTGCTTAGCGT	592
361	Db	GACTGGTGAGCTGAAACAGTATCAAGCTGCAGAGTGAGATTGGCAAGGGTGCTTAGCGT	420
593	Qy	GTGGTCAGGCTGGCCCTAACAGAAAGTGAAGACAGACACTATGCAATGAAAGTCTTTTCC	652
421	Db	GTGGTCAGGCTGGCCCTAACAGAAAGTGAAGACAGACACTATGCAATGAAAGTCTTTTCC	480
653	Qy	AAAAAGAAATTACTGAAGCAGTATGAGTTTTCACAGTGCCTCCCGGAGAGGGTCCCGAG	712
481	Db	AAAAAGAAATTACTGAAGCAGTATGAGTTTTCACAGTGCCTCCCGGAGAGGGTCCCGAG	540
713	Qy	GGTGGCCAGGGAGCACAGCAAGCAGCTGTCTCCCTCGAGCGGGTGTTACCAAGGAGATT	772
541	Db	GGTGGCCAGGGAGCACAGCAAGCAGCTGTCTCCCTCGAGCGGGTGTTACCAAGGAGATT	600
773	Qy	GCCATCCTGAAGAAGCTGGACCAAGTGAATGTGGTCAAACTGATCGAGGTCCTGGATGAC	832
601	Db	GCCATCCTGAAGAAGCTGGACCAAGTGAATGTGGTCAAACTGATCGAGGTCCTGGATGAC	660
833	Qy	CGAGCTGAGGACAACTCTATTGTGTGTTGACCTCTCGAAGAGGGGCCGTCATGGAA	892
661	Db	CGAGCTGAGGACAACTCTATTGTGTGTTGACCTCTCGAAGAGGGGCCGTCATGGAA	720
893	Qy	GTCCCTGTGACAAAGCCCTTCTCGAGGAGCAAGCTCGCTCTACCTCGCGGACGTCATC	952
721	Db	GTCCCTGTGACAAAGCCCTTCTCGAGGAGCAAGCTCGCTCTACCTCGCGGACGTCATC	780
953	Qy	CTGGGCTCGAGTACTTGTGACTGCCAGAGATCGTCCACAGGACATCAAGCCATCCAAC	1012
781	Db	CTGGGCTCGAGTACTTGTGACTGCCAGAGATCGTCCACAGGACATCAAGCCATCCAAC	840
1013	Qy	CTGCTCTGGGGATGATGGGCAAGTGAAGATCGCCGACTTTGGCGGTCAAGCAACAGTTT	1072
841	Db	CTGCTCTGGGGATGATGGGCAAGTGAAGATCGCCGACTTTGGCGGTCAAGCAACAGTTT	900
1073	Qy	GAGGGGAAAGACGCTCAGCTGTCCAGACCGCGGGGAAACCCAGATTCATGGGCCCGGAG	1132
901	Db	GAGGGGAAAGACGCTCAGCTGTCCAGACCGCGGGGAAACCCAGATTCATGGGCCCGGAG	960
1133	Qy	GCCATTCTGATTTCCGCGCAGAGCTTCAGTGGGAAGGCGTTGGATGTATGGGCCACTGGC	1192
961	Db	GCCATTCTGATTTCCGCGCAGAGCTTCAGTGGGAAGGCGTTGGATGTATGGGCCACTGGC	1020
1193	Qy	GTACGTTGTACTGCTTTGTCTATGGGAAGTGCCCATTCATCGACGATTCATCTTGGCC	1252
1021	Db	GTACGTTGTACTGCTTTGTCTATGGGAAGTGCCCGTTTCATCGACGATTCATCTTGGCC	1080
1253	Qy	CTCCAAGGAGATCAAGATGAGCCGTGGTGTTCCTGAGGAGCCAGAGAAATCAGCGAG	1312
1081	Db	CTCCAAGGAGATCAAGATGAGCCGTGGTGTTCCTGAGGAGCCAGAGAAATCAGCGAG	1140
1313	Qy	GAGCTCAAGGACCTGATTCCTGAAGATGTTTAGACAAGAAATCCCGAGAAGATTTGGGGTG	1372

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Db 1141 GAGCTCAAGGACCTGATCTCTGAAGATTTAGACAAGAAATCCCGAGACGAGAATTTGGGGTG 1200
QY 1373 CCAGACATCAAGTTGCACCTTTGGGTGACCAAGAAACGGGGAGAGCCCCCTTCTTCGGAG 1432
Db 1201 CCAGACATCAAGTTGCACCTTTGGGTGACCAAGAAACGGGGAGAGCCCCCTTCTTCGGAG 1260
QY 1433 GAGGAGCATCTGAGCGTGTGTGAGGTGACAGAGGGGGAGGTTAAGAACTCAGTCAGGGTTC 1492
Db 1261 GAGGAGCATCTGAGCGTGTGTGAGGTGACAGAGGGGGAGGTTAAGAACTCAGTCAGGGTTC 1320
QY 1493 ATCCCCAGCTGACACACGCTGATCTCTGGTGAAGTCCATGCTCAGGAAGGTTCCCTTTGGG 1552
Db 1321 ATCCCCAGCTGACACACGCTGATCTCTGGTGAAGTCCATGCTCAGGAAGGTTCCCTTTGGG 1380
QY 1553 AACCCGTTTGAGCCCCCAGGACACGAGGGAAGAGCGATCCATGCTCTCCAGGAACCTTA 1612
Db 1381 AACCCGTTTGAGCCCCCAGGACACGAGGGAAGAGCGATCCATGCTCTCCAGGAACCTTA 1440
QY 1613 CTGGTGAAGAGGGTTGGTGAAGGGGGCAAGAGCCAGAGCTCCCGGGCGTCCAGGAA 1672
Db 1441 CTGGTGAAGAGGGTTGGTGAAGGGGGCAAGAGCCAGAGCTCCCGGGCGTCCAGGCT 1500
QY 1673 GACGA 1677
Db 1501 TACCA 1505

RESULT 11
US-10-391-364-43
; Sequence 43, Application US/10391364
; Publication No. US20040121349A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Meyers, Rachel E.
; APPLICANT: Carroll, Joseph M.
; APPLICANT: Cook, William James
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: Weich, Nadine S.
; APPLICANT: Bandaru, Rajasekhar
; TITLE OF INVENTION: NOVEL 27877, 18080, 14081, 32140, 50352,
; TITLE OF INVENTION: 16658, 14223, 16002, 50566, 65552 AND 65577 MOLECULES AND
; TITLE OF INVENTION: USES THEREFOR
; FILE REFERENCE: MP103-0190NM1M
; CURRENT APPLICATION NUMBER: US/10/391,364
; CURRENT FILING DATE: 2003-03-18
; PRIOR APPLICATION NUMBER: US 09/950,370
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: US 60/231,084
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: US 10/294,039
; PRIOR FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 60/338,587
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 10/266,035
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: US 60/328,198
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: US 09/717,926
; PRIOR FILING DATE: 2000-11-21
; PRIOR APPLICATION NUMBER: US 60/214,707
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: US 10/268,036
; PRIOR FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US 60/327,820
; PRIOR FILING DATE: 2001-10-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 43
; LENGTH: 1686
; TYPE: DNA
; ORGANISM: Homo sapiens
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; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1) ... (1686)
US-10-391-364-43

Query Match 68.1%; Score 1490.6; DB 17; Length 1686;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 1496; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 173 ATGAGGGGGTCCAGCTGTCTGCTCCAGAGATCCTCGGGCAGAGCTGGTGAACCGGGTG 232
Db 1 ATGAGGGGGTCCAGCTGTCTGCTCCAGAGATCCTCGGGCAGAGCTGGTGAACCGGGTG 60
QY 233 GCAGCCATCGATGTGACTCCTCTGGAGGAGGAGATGGTGGCCAGAGCCTACTAGAAAC 292
Db 61 GCAGCCATCGATGTGACTCCTCTGGAGGAGGAGATGGTGGCCAGAGCCTACTAGAAAC 120
QY 293 GGTGTGGACCCCCACCAAGGGCCAGAGTGGCTCTGTGATCCCTGGCAGTACTTCAAGA 352
Db 121 GGTGTGGACCCCCACCAAGGGCCAGAGTGGCTCTGTGATCCCTGGCAGTACTTCAAGA 180
QY 353 CTGCTCCAGCCCGGCTTAGCTCTCAGCCAGGAAGCTTTCCCTACAGAGGGCCAGCA 412
Db 181 CTGCTCCAGCCCGGCTTAGCTCTCAGCCAGGAAGCTTTCCCTACAGAGGGCCAGCA 240
QY 413 GGAAGCTATCTGGAGGGCGCAGGCTGGGGCTTTATGCCAGGGGCTTCCAGGCACATCTCC 472
Db 241 GGAAGCTATCTGGAGGGCGCAGGCTGGGGCTTTATGCCAGGGGCTTCCAGGCACATCTCC 300
QY 473 CCCGGGGCTTGGCGGAGGCCACCATCGAGTCCCAACAGTGGGCCATCTCAGATCGAGAG 532
Db 301 CCCGGGGCTTGGCGGAGGCCACCATCGAGTCCCAACAGTGGGCCATCTCAGATCGAGAG 360
QY 533 GACTGCTGACGTGAACACAGTACAAGCTGCAGAGTGAGATTGGCAAGGGTGCCTACCGT 592
Db 361 GACTGCTGACGTGAACACAGTACAAGCTGCAGAGTGAGATTGGCAAGGGTGCCTACCGT 420
QY 593 GTGTGAGGCTGGGCTTACAACGAAAGTGAAGACAGACACTATGCAATGAAAGTCTCTTTC 652
Db 421 GTGTGAGGCTGGGCTTACAACGAAAGTGAAGACAGACACTATGCAATGAAAGTCTCTTTC 480
QY 653 AAAAAGATTACTGACAGCAGTATGGCTTTCAGTGCCTCCCTCCCGAGAGGGTCCAG 712
Db 481 AAAAAGATTACTGACAGCAGTATGGCTTTCAGTGCCTCCCTCCCGAGAGGGTCCAG 540
QY 713 GCTGCCAGGAGGACCAAGCAGCTGCTGCCCTTGGAGCGGTGTGTACAGAGATT 772
Db 541 GCTGCCAGGAGGACCAAGCAGCTGCTGCCCTTGGAGCGGTGTGTACAGAGATT 600
QY 773 GCCATCTGAAGAAGCTGGACCAAGTGAATGTGGTCAAACTGATCGAGGTCTTGGATGAC 832
Db 601 GCCATCTGAAGAAGCTGGACCAAGTGAATGTGGTCAAACTGATCGAGGTCTTGGATGAC 660
QY 833 CCAGCTGAGGACCAACCTCTATTGGTGTGACCTCTGAGAAAGGGGCCCGTCAAGAA 892
Db 661 CCAGCTGAGGACCAACCTCTATTGGTGTGACCTCTGAGAAAGGGGCCCGTCAAGAA 720
QY 893 GTGCCCTGTGACAAGCCCTTCTCGAGGAGCAAGCTGCCTCTTACCTGCGGGAGTCAATC 952
Db 721 GTGCCCTGTGACAAGCCCTTCTCGAGGAGCAAGCTGCCTCTTACCTGCGGGAGTCAATC 780
QY 953 CTGGGCTCTCGAGTACTTGCATCTGCCAGAGAATCGTCCACAGGGACATCAAGCCATCCAAC 1012
Db 781 CTGGGCTCTCGAGTACTTGCATCTGCCAGAGAATCGTCCACAGGGACATCAAGCCATCCAAC 840
QY 1013 CTGCTCTGGGGATGATGGGCAAGTGAAGTCCCGGACTTTTGGCGTCAGCAACAGTTT 1072
Db 841 CTGCTCTGGGGATGATGGGCAAGTGAAGTCCCGGACTTTTGGCGTCAGCAACAGTTT 900
QY 1073 GAGGGGAACGACGCTCAGCTGTCAGCAGCGCGGGACCCCGAGCATTCATGGCCCCCGAG 1132
Db 901 GAGGGGAACGACGCTCAGCTGTCAGCAGCGCGGGAAACCCCGAGCATTCATGGCCCCCGAG 960
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Qy 1133 GCCATTCTGATTCGGCCAGAGCTTCAGTGGGAAGCCCTTGATGTATGGGCCACTGGC 1192
Db 961 GCCATTCTGATTCGGCCAGAGCTTCAGTGGGAAGCCCTTGATGTATGGGCCACTGGC 1020
Qy 1193 GTCACGTTGTACTGCTTTGTCTATGGGAAGTGCCTTATTCACACGATTTTCATCTCTGGCC 1252
Db 1021 GTCACGTTGTACTGCTTTGTCTATGGGAAGTGCCTTATTCACACGATTTTCATCTCTGGCC 1080
Qy 1253 CTCACAGGAAGATCAAGATGAGCCCGTGTGTTCTCTGAGGAGCCAGAAATCAGCGAG 1312
Db 1081 CTCACAGGAAGATCAAGATGAGCCCGTGTGTTCTCTGAGGAGCCAGAAATCAGCGAG 1140
Qy 1313 GAGCTCAAGACCTGATCCTGAAGATCTTAGACAAGNAATCCGAGACGAGAAATGGGGTG 1372
Db 1141 GAGCTCAAGACCTGATCCTGAAGATCTTAGACAAGNAATCCGAGACGAGAAATGGGGTG 1200
Qy 1373 CCAGACATCAAGTTGACCCCTTGGGTGACCAAGAACGGGAGGAGCCCTTCTCTCGGAG 1432
Db 1201 CCAGACATCAAGTTGACCCCTTGGGTGACCAAGAACGGGAGGAGCCCTTCTCTCGGAG 1260
Qy 1433 GAGGAGACTGACGCGTGTGGAGTGACAGAGGGGAGGTTAAGAACTCAGTCAGGCTC 1492
Db 1261 GAGGAGACTGACGCGTGTGGAGTGACAGAGGGGAGGTTAAGAACTCAGTCAGGCTC 1320
Qy 1493 ATCCGAGCTGGACCAAGCTGATCCTGCTGAAGTCCATGCTGAGGAAGCGTTCCTTTGGG 1552
Db 1321 ATCCGAGCTGGACCAAGCTGATCCTGCTGAAGTCCATGCTGAGGAAGCGTTCCTTTGGG 1380
Qy 1553 AACCCGTTTTCAGGCCCCAGGACGAGGAGGAGGAGGATCCATGCTGCTCCAGGAAACCTA 1612
Db 1381 AACCCGTTTTCAGGCCCCAGGACGAGGAGGAGGAGGATCCATGCTGCTCCAGGAAACCTA 1440
Qy 1613 CTGGTGAAGAAAGGTTTGGTGAAGGGGGCAAGAGCCAGAGTCCCGGCGTCCAGGAA 1672
Db 1441 CTGGTGAAGAAAGGTTTGGTGAAGGGGGCAAGAGCCAGAGTCCCGGCGTCCAGGCT 1500
Qy 1673 GACGA 1677
Db 1501 TACCA 1505

RESULT 12
US-10-092-900A-57
; Sequence 57, Application US/10092900A
; Publication No. US20040043382A1
; GENERAL INFORMATION:
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Taupier Jr., Raymond J.
; APPLICANT: Pena, Carol E.A.
; APPLICANT: Li, Li
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Ji, Weizhen
; APPLICANT: Gorman, Linda
; APPLICANT: Miller, Charles E.
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Patturajan, Meera
; APPLICANT: Gangolli, Esha A.
; APPLICANT: Vernet, Corine A.M.
; APPLICANT: Guo, Xiaojia Sasha
; APPLICANT: Tchernev, Velizar T.
; APPLICANT: Fernandes, Elma R.
; APPLICANT: Casman, Stacie J.
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Liu, Yi
; APPLICANT: Anderson, David W.
; APPLICANT: Spaderna, Steven K.
; APPLICANT: Catterton, Elina
; APPLICANT: Leite, Mario W.
; APPLICANT: Zhong, Haihong

; APPLICANT: Alsobrook, John P.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Burgess, Catherine E.
; TITLE OF INVENTION: No. US20040043382A1e1 Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-290C
; CURRENT APPLICATION NUMBER: US/10/092,900A
; CURRENT FILING DATE: 2002-03-07
; PRIOR APPLICATION NUMBER: USSN 60/274,322
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: USSN 60/283,675
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: USSN 60/338,092
; PRIOR FILING DATE: 2001-12-03
; PRIOR APPLICATION NUMBER: USSN 60/274,281
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: USSN 60/274,191
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: USSN 60/325,681
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: USSN 60/304,354
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: USSN 60/279,995
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: USSN 60/294,899
; PRIOR FILING DATE: 2001-05-31
; PRIOR APPLICATION NUMBER: USSN 60/287,424
; PRIOR FILING DATE: 2001-04-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 768
; SEQ ID NO 57
; LENGTH: 1725
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (52)..(1681)
US-10-092-900A-57

Query Match 67.4%; Score 1475.8; DB 13; Length 1725;
Best Local Similarity 93.0%; Pred. No. 0;
Matches 1604; Conservative 0; Mismatches 7; Indels 114; Gaps 1;
Qy 122 GCGCCAGGTTCCCAACAGGCTACGAGAGAACCCCTTGACTGAAGCAATGGAGGG 181
Db 1 GCGCCAGGTTCCCAACAGGCTACGAGAGAACCCCTTGACTGAAGTAATGGAGGG 60
Qy 182 GGTCCAGCTCTCTGCTGCCAGGATCCTCGGGCAGAGCTGTAGAAACGGGTGGCAGCCATC 241
Db 61 GGTCCAGCTCTCTGCTGCCAGGATCCTCGGGCAGAGCTGTAGAAACGGGTGGCAGCCATC 120
Qy 242 GATGTGACTCATTGGAGGAGGAGAGTGGTGGCCAGAGCTACTAGAAACGGGTGGAG 301
Db 121 GATGTGACTCATTGGAGGAGGAGAGTGGTGGCCAGAGCTACTAGAAACGGGTGGAG 180
Qy 302 CCCACACAGGCGCAGAGCTGCTCTGTGATCCCTGGCAGTACTTCAAGACTGCTCCCA 361
Db 181 CCCACACAGGCGCAGAGCTGCTCTGTGATCCCTGGCAGTACTTCAAGACTGCTCCCA 240
Qy 362 GCCCGGCTAGCTTCTCAGCCAGGAAGCTTTCCTTACAGGAGCGCCAGCAGAGAGTAT 421
Db 241 GCCCGGCTAGCTTCTCAGCCAGGAAGCTTTCCTTACAGGAGCGCCAGCAGGAAGTAT 300
Qy 422 CTGGAGGCGCAGAGTGGGCTTATGCCACGGGCGCTGCCAGCCACATCTCCCCCGGGCC 481
Db 301 CTGGAGGCGCAGAGTGGGCTTATGCCACGGGCGCTGCCAGCCACATCTCCCCCGGGCC 360
Qy 482 TGGCAGAGGCCACCATCGAGTCCCAACAGTGGCCATCTCAGATGAGAGGACTGCGTG 541
Db 361 TGGCAGAGGCCACCATCGAGTCCCAACAGTGGCCATCTCAGATGAGAGGACTGCGTG 420
Qy 542 CAGCTGAACAGGTACAAAGCTGCGAGTGGAGTTGGCAAGGGTGCCTACGGTGTGGTGG 601

Db 421 CAGCTGAACAGTCAAGCTGCAGAGTGAGATTGGCAAGGGTGCCCTACGGTGTGTGAGG 480
QY 602 TTGGCTTCAACGAAAGTGAAGACGACACTATGCAATGAAAGTCTTTTCCAAAGAGAG 661
Db 481 CTGGCTTCAACGAAAGTGAAGACGACACTATGCAATGAAAGTCTTTTCCAAAGAGAG 540
QY 662 TTACTGAGCAGTATGCTTTCCAGTGCCTCTCCCGAGAGGGTCCAGGCTGCCAG 721
Db 541 TTACTGAGCAGTATGCTTTCCAGTGCCTCTCCCGAGAGGGTCCAGGCTGCCAG 600
QY 722 GGAGCACCAGCAAGCAGCTGTGCTGCCCTCGAGCGGGTGTACAGAGAGATTCCTATCCTG 781
Db 601 GGAGCACCAGCAAGCAGCTGTGCTGCCCTCGAGCGGGTGTACAGAGAGATTCCTATCCTG 660
QY 782 AAGAGCTGGACCAAGTGAATGTGTCAAACTGATCGAGGCTCTCGATGACCCAGCTGAG 841
Db 661 AAGAGCTGGACCAAGTGAATGTGTCAAACTGATCGAGGCTCTCGATGACCCAGCTGAG 720
QY 842 GACACCTCTATTG----- 856
Db 721 GACACCTCTATTG----- 856
QY 857 ----- 856
Db 781 ATCGCAGAGTCCACTCCCTGCTTCCCTCTGAGCAGCAAGCAGTGGATCCAGTGGGCT 840
QY 857 -----GTGTTGACTCTCTGAGAAAGGGGCCCGTCAATGGAAGTGCCTGTGACAG 907
Db 841 GCGCGCTCAGTGTGACTCTCTGAGAAAGGGGCCCGTCAATGGAAGTGCCTGTGACAG 900
QY 908 CCTTCTCGAGGACGAGCTGCCTCTACCTCGGGAGCTCATCTGGGCTCAGTAC 967
Db 901 CCTTCTCGAGGACGAGCTGCCTCTACCTCGGGAGCTCATCTGGGCTCAGTAC 960
QY 968 TTGCACTGCCAAGATCGTCCACAGGACATCAAGCCATCAACTGCTCTCGGGGAT 1027
Db 961 TTGCACTGCCAAGATCGTCCACAGGACATCAAGCCATCAACTGCTCTCGGGGAT 1020
QY 1028 GATGGGCGTGAAGATCGCGCACTTTGGCGTCAAGCAACAGTTTGGGGGAAACGACGT 1087
Db 1021 GATGGGCGTGAAGATCGCGCACTTTGGCGTCAAGCAACAGTTTGGGGGAAACGACGT 1080
QY 1088 CAGCTGTCCAGCAGCGCGGACCCAGCATTCATGGCCCGGAGGCCATTTCTGATTC 1147
Db 1081 CAGCTGTCCAGCAGCGCGGAAACCCAGCATTCATGGCCCGGAGGCCATTTCTGATTC 1140
QY 1148 GCGCAGAGCTTCAGTGGGAAGGCTTTGGATGTATGGGCCACTGGCGTCAAGTTGACTGC 1207
Db 1141 GCGCAGAGCTTCAGTGGGAAGGCTTTGGATGTATGGGCCACTGGCGTCAAGTTGACTGC 1200
QY 1208 TTTGTTATGGGAAGTGCCTCAATCAAGCAATTTTCATCTGGCCCTCCACAGGAAGATC 1267
Db 1201 TTTGTTATGGGAAGTGCCTCAATCAAGCAATTTTCATCTGGCCCTCCACAGGAAGATC 1260
QY 1268 AAGATGAGCGCTGCTTTCTTCTGAGGCGCAGAAATTCAGCAGGAGCTCAGGACCTG 1327
Db 1261 AAGATGAGCGCTGCTTTCTTCTGAGGCGCAGAAATTCAGCAGGAGCTCAGGACCTG 1320
QY 1328 ATCTCTGAAGATGTTAGACAAGAAATCCCGAGACGAAATTTGGGTGCCAGACATCAAGTTG 1387
Db 1321 ATCTCTGAAGATGTTAGACAAGAAATCCCGAGACGAAATTTGGGTGCCAGACATCAAGTTG 1380
QY 1388 CACCTTGGGTGACCAAGAACGGGAGAGGAGCCCTTCTTCTGGAGGAGGACCTTCGACG 1447
Db 1381 CACCTTGGGTGACCAAGAACGGGAGAGGAGCCCTTCTTCTGGAGGAGGACCTTCGACG 1440
QY 1448 GTGTGGAGGTCACAGAGGGGAGGTTAAGAACTCAGTCAAGCTCATCCAGCTGGACC 1507
Db 1441 GTGTGGAGGTCACAGAGGAGGAGGTTAAGAACTCAGTCAAGCTCATCCAGCTGGACC 1500
QY 1508 ACGGTGATCTCTGTAAGTCCATGTCTGAGGAAGCGTTCCTTTGGGAACCCGTTTGAGGCC 1567
Db 1501 ACGGTGATCTCTGTAAGTCCATGTCTGAGGAAGCGTTCCTTTGGGAACCCGTTTGAGGCC 1560

RESULT 13

US-10-295-027-1138
; Sequence 1138, Application US/10295027
; Publication No. US20030232350A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glyme, Richard
; APPLICANT: Hevezi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; FILE OF INVENTION: Methods of Screening for Modulators of Cancer
; FILE REFERENCE: 018501-012500US
; CURRENT APPLICATION NUMBER: US/10/295,027
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 09/663,733
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/335,394
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/332,464
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/334,393
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/340,376
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/347,211
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/347,349
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/355,250
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/356,714
; PRIOR FILING DATE: 2002-02-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1138
; LENGTH: 5611
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-295-027-1138

Query Match 29.8%; Score 653.6; DB 16; Length 5611;
Best Local Similarity 70.7%; Pred. No. 2.2e-169;
Matches 899; Conservative 0; Mismatches 369; Indels 4; Gaps 2;
QY 439 GCCTTATGCCAGGGGCTTGCAGCCACATCTCCCGCGGCTTGGGAGGAGCCCAT 498
Db 1201 GCCCTACTCACCGCTCAGCTCCCGCAGTCTCGCTCGCTGCCCGCGGCGGACAGT 1260
QY 499 CGAGTCCACACGCTGGCCATCTCAGATGCAGAGACTGCGTGCAGTGAACCGATCA 558

Db 1261 GGAGTCTCACCACGCTCTCCATCAGCGGTATGAGGACTGTGTGACGTGAATCAGTATAC 1320
Qy 559 GCTGCGAGTGAAGATTGGCAAGGTTGCTACGGTGTGGTGAAGCTGCTGTACCAACGAAG 618
Db 1321 CCTGAAGTGAATTTGAAAGGGCTCTATGGTGTGCTCAAGTTGGCTTACATGAAA 1380
Qy 619 TGAAGACAGACATATGCRATGAAGTCTTTCRAAAGAAAGTTACTGAAGCAGTATGG 678
Db 1381 TGACAAATACCTACTATGCAATGAAGGTGCTGTCCAAAAGAAAGCTGATCCGGCGGCCG 1440
Qy 679 CTTTTCACGTCGCGCTCCCGCGAGAGGTCCTCAGGCTGCCAGGGAGCACCAAGCA 738
Db 1441 CTTTTCACGTCGCGCTCCACCGGAGGACCGCGCCAGCTCTCTGGAGCTGCATCCAGCC 1500
Qy 739 GCTGCTGCCCTCGAGGCGGTGTACAGAGATTGCCATCCTGAAGAACTGTGACCAAGT 798
Db 1501 CAGGGGCCCCATTGAGCAGGTGTACCAAGAAATGGCCATCTCAAGAAAGCTGGACCAACC 1560
Qy 799 GAATGTGGTCAAACTGATCAGGTCCTGGATGACCCAGCTGAGGACAACTCTATTGGT 858
Db 1561 CAATGTGGTGAAGCTGGTGGAGTCTCTGGATGACCCCAATGAGGACCATCTGTACATGGT 1620
Qy 859 GTTTGACCTCTCAGAAAGGGGCGCGTCATGGAAGTCCCTGTGACAAAGCCCTTCTCGGA 918
Db 1621 GTTCGAAGTGTCAACCAAGGCGCGTGTGGAAGTSCCCACCTCAACCACTCTCTGA 1680
Qy 919 GAGCAAGCTGCGCTCTACTGCGGGAGCTCATCTGGGCTCGAGTACTTGACTGCCA 978
Db 1681 AGACCAGGCGCGTTTCTACTTCCAGGATCTGATCAAAAGGATCGAGTACTTACACTACCA 1740
Qy 979 GAAGATCGTCCACAGGACATCAAGCCATCAACCTGCTCTGGGGATGATGGGACGT 1038
Db 1741 GAAGATCATCACCGTGACATCAAACTTCAACCTCTGTCGGAGAAATGAGGACAT 1800
Qy 1039 GAAGATCGCGACTTTGGCGTCAAGCAACCAAGTTTGGGGAAACAGCCTCAGCTGTCCAG 1098
Db 1801 CAAGATCGCTGACTTTGGTGTGACATGAATCAAGGGCAGTGAACGCGCTCTCTCAA 1860
Qy 1099 CAGCGGGAAACCCAGCATTCATGGCCCGGAGGCCATTCTGTGATTCGGCCAGACTT 1158
Db 1861 CACCGTGGGACGCGCCCTTCAATGGCACCCGAGTGTCTCTGTAGACCCGCAAGATCTT 1920
Qy 1159 CAGTGGAAAGCCCTTGTGATGTGGGCACTGGGTCACGTTGTACTGCTTTGTCTATGG 1218
Db 1921 CTCCTGGAAAGCCCTTGTGATGTGGGCAATGGGTGTGACATATCTGCTTTGTCTTGG 1980
Qy 1219 GAAGTGCCCAATTCACGACGATTTCACTCTGGCCCTCCACAGGAAGATCAAGATGAGCC 1278
Db 1981 CCAGTGCCCAATTCATGACGAGCGGATCATGTGTTTACACAGTAAGATCAAGAGTCAGGC 2040
Qy 1279 CGTGGTGTCTTCTGAGGACGAGAAATCAGGAGGAGCTCAGGACCTGATCTCTGAAGAT 1338
Db 2041 CCTGGAAATTTCCAGACGCGCGCATAGCTGAGGACTTGAAGGACCTGATCAACCCGTAT 2100
Qy 1339 GTTAGACAAGAAATCCCGACAGAGAAATTTGGGTGCCAGACATCAAGTTGCACCCCTGGGT 1398
Db 2101 GCTGGACAGAAACCCCGAGTCAGGATCGTGTGTGCGGAAATCAAGCTGCACCCCTGGGT 2160
Qy 1399 GACCAAGAACGGGAGGAGCCCTTCTTCTGGAGGAGAGCACTGACAGCGTGTGGAGGT 1458
Db 2161 CACGAGGCATGGGCGGAGCGTTTGGCTCGGAGGATGAGAACTGCACGCTGTGCGAAGT 2220
Qy 1459 GACAGGGGGAGGTAAAGACTCAGTCAGGCTCATCCGAGCTGAGACCAAGCTGATCCT 1518
Db 2221 GACTGAAGAGAGGTGAGAACTCAGTCAAAACATTTCCAGCTTGGCAACCGGTATCCT 2280
Qy 1519 GGTGAAGTCCAATGCTGAGGAAGCGTCTCTTTGGAAACCCGTTTGGAGCCCGAGCAAG 1578
Db 2281 GGTGAAGACCAATGATACGTAAGCTCTCTTTGGGAAACCCATTCAGGGC---AGCCGGCG 2337
Qy 1579 GGAAGAGGATCCATGTCTGCTCAGGAACCTACTGCTGGAAGAGGGTTTGTGAGG 1638
Db 2338 GGAGGAACGCTCACTGTGAGCGCTGGGAACTTCTGTCAACCAAAAAACCAACCGGAATG 2397

Qy 1639 GGSCAAAGAGCCAGAGCTCCCGCGTCCAGGAAGACGAGGCTGCATCTCTGAGCCCTGC 1698
Db 2398 TGAGTCCCTGTCTGAGCT-CAAGGAAGCAAGGAGGAGGAGCAACCTTCCAGGGCACCAC 2456
Qy 1699 ATCACCACCGGG 1710
Db 2457 CCGCCCCCGGTG 2468

RESULT 14

US-10-316-124-7
; Sequence 7, Application US/10316124
; Publication No. US20030152574A1
; GENERAL INFORMATION:
; APPLICANT: Logan, Thomas Joseph
; APPLICANT: Chun, Miyoung
; TITLE OF INVENTION: METHODS AND COMPOSITIONS TO TREAT
; TITLE OF INVENTION: CARDIOVASCULAR DISEASE USING 1419, 58765, AND 2210
; FILE REFERENCE: MPI01-291PIRM
; CURRENT APPLICATION NUMBER: US/10/316,124
; CURRENT FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: 60/339,995
; PRIOR FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 4427
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-316-124-7

Query Match 29.7%; Score 651.2; DB 15; Length 4427;
Best Local Similarity 71.3%; Pred. No. 9.5e-169;
Matches 873; Conservative 0; Mismatches 348; Indels 3; Gaps 1;

Qy 439 GCCTTAGCCACCGGGGCTGCCAGCCACATCTCCCCCGGGCCCTGGCGGAGGCCACCAT 498
Db 360 GCCTTACTACCGCTCAGCTCCCGCAGTCTCTGCTCGCTGCGCTGCCCGCGGCGACAGT 419
Qy 499 CGAGTCCCAACCGTGGCCATCTCAGATCAGAGGACTGTGTGAGCTGAACCAAGTACAA 558
Db 420 GGAAGTCTCACCGCTCTCCATCACGGGTATGCGAGGACTGTGTGAGCTGAATCAGTATAC 479
Qy 559 GCTGCGAGTGAAGTTGGCAAGGTCCTACGCTGTGTGAGGCTGCCCTACACGAAG 618
Db 480 CCTGAAGGATGAATTTGAAAGGCTCCTATGGTGTGCTCAAGTTGGCTTACATGAAA 539
Qy 619 TGAAGACAGACACTATGCAATGAAAGTCTTTTCCAAAAAGAAAGTTACTGAAGCAGTATGG 678
Db 540 TGACAAATACCTACTATGCAATGAAGGTGCTGTCCAAAAAGAGCTGATCCGGCAGGCCG 599
Qy 679 CTTTTCACGTCGCGCTCCCGCGAGAGGTCCTCAGGCTGCCCGAGGAGGACCGCAAGCA 738
Db 600 CTTTTCACGTCGCGCTCCACCGGAGGACCCCGCCAGCTCCTGGAGGCTGCATCCAGCC 659
Qy 739 GCTGCTGCCCTCGAGCGGCTGTACAGGAGATTGCCATCCTGAAGAGCTGACCAAGCT 798
Db 660 CAGGGGCCCCATTGAGCAGGTGTACCAAGAAATTTGCCATCTCAAGAGCTGACCAACC 719
Qy 799 GAATGTGTCAAACTGATCGAGGTCTCTGGATGACCCAGCTGAGGACAACTCTATTGGT 858
Db 720 CAATGTGTGAAGCTGTGTGAGGTCTCTGGATGACCCCAATGAGACCATCTGTACATGGT 779
Qy 859 GTTTGACCTCTGAGAAAGGGCCGCTCATGGAGTGCCTGTGACAAAGCCCTTCTCGGA 918
Db 780 GTTCGAAGTGGTCAACCAAGGGCCCGGTGATGGAAGTGCACCCCTCAACCACTCTCTGA 839
Qy 919 GGAAGCAAGCTCGGCTCTTACCTGCGGAGCTCATCTCTGGGCTCGAGTACTTTGCACTGCA 978
Db 840 AGACCAGGCGCGTTTCTTACTTCCAGGATCTGATCAAGAGGATCGAGTACTTACACTACCA 899
Qy 979 GAAGATCGTCCACAGGAGACATCAAGCCATCCAACTCTCTCTGGGGGATGATGGGACGT 1038


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||||| 900 GAAGATATCCACCGTGACATCAAACTTCCAACTCTCTGGTCGGAGAAAGATGGGCACAT 959
||||| 1039 GAAGATCGCCGACTTTGGCGTCAGCAACAGATTTGAGGGGAAACGACGCTCAGCTGTCCAG 1098
||||| 960 CAAGATCGCTGACTTTGGTGTGAGCAATGAATTCAGGGCAGTGAGCGCTCTCTCCAA 1019
||||| 1099 CAGCGGGGAAACCCAGCATTCATGGCCCCCGAGGCGCATTTCTGATTCGGGCGAAGCTT 1158
||||| 1020 CACCGTGGGCAACCGCGCTTATGGCACCCGAGTGGCTCTCTGAGACCCGCAAGATCTT 1079
||||| 1159 CAGTGGGAAGGCTTTGGATGATGGGCACTGGCGCTCAGCTGTGATCTGCTTTGTCTATGG 1218
||||| 1080 CTCGGGAAGGCTTTGGATGATTTGGGCCATGGGTGACACTATCTGCTTTGTCTTTGG 1139
||||| 1219 GAAGTGCCCATTCATCGACGATTTTCATCTCGCCCTCCACAGGAAGATCAAGAAATGAGCC 1278
||||| 1140 CCAGTGCCCATTCATGGACGCGGATCATGTGTTTACACAGTAAGATCAAGATCAGGC 1199
||||| 1279 CGTGTGTTTCTGAGGAGCCAGAAATCAGCGAGGACTCAAGGACCTGATCCTGAAAGAT 1338
||||| 1200 CCTGGAAATTCAGACCCAGCCGACATAGCTGAGGACTTGAAGGACCTGATCACCCGTAT 1259
||||| 1339 GTTAGACAAGAAATCCGAGAACAGAAATGGGGTGGCCAGACATCAAGTTGCACCCCTTGGT 1398
||||| 1260 GCTGACAAAGAACCCCGAGTCGAGATCGTGTGCGGAAATCAAGCTGCACCCCTGGGT 1319
||||| 1399 GACCAAGAACCGGGAGGAGCCCTTCTCTCGGAGGAGGAGCACTGACGCTGGTGAGGT 1458
||||| 1320 CACGAGGCATGGGCGGAGCGCTTCCGCTCGGAGGATGAGRACTGACCGCTGTCGAAGT 1379
||||| 1459 GACAGAGGGGAGGTAAAGAACTGATCAGGCTCATCCCCAGCTGGAACACGGTGAATCT 1518
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||||| 1557 TGAGTCCCTGTGTGAGCTCAAGGG 1580
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US-10-316-124-8
; Sequence 8, Application US/10316124
; Publication No. US20030152574A1
; GENERAL INFORMATION:
; APPLICANT: Logan, Thomas Joseph
; APPLICANT: Chun, Miyeung
; TITLE OF INVENTION: METHODS AND COMPOSITIONS TO TREAT
; FILE OF INVENTION: CARDIOVASCULAR DISEASE USING 1419, 58765, AND 2210
; FILE REFERENCE: MP101-291PIRM
; CURRENT APPLICATION NUMBER: US/10/316,124
; CURRENT FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: 60/339,995
; PRIOR FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 4427
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (127)....(1653)
US-10-316-124-8
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Query Match 29.7%; Score 651.2; DB 15; Length 4427;
Best Local Similarity 71.3%; Pred. No. 9.5e-169;
Matches 873; Conservative 0; Mismatches 348; Indels 3; Gaps 1;

QY 439 GCCTTATGCCAGGGGCTGGCCAGGCACATCTCCCCCGGGCTGGCGAGGCGCCACCAT 498
DB 360 GGCCTACTACCCCGTCACTCCCGCAGTCTCTGGCTGGCTGCCCGCGCGCCGACAGT 419
QY 499 CGAGTCCCAACACGCTGGCCATCTCAGATGCAGAGGACTGCGTGACAGTGAACACGATACAA 558
DB 420 GGAGTCTCACCAGCTCTCAATCACGGGTATCAGAGACTGTGTGAGCTGAATCAGTATAC 479
QY 559 GCTGACAGTGAATGGCAAGGGTCCCTAOGTGTGTGAGGCTGGCTCAACGGAAG 618
DB 480 CCTGAAGATGAATTTGAAAGGGCTCTATGTTGCTCAAGTTGGCTCAATGAAAA 539
QY 619 TGAACACAGACACTATGCAATGAAGTCTTTCCAAAAGAGTTACTGAGCAGTATGG 678
DB 540 TGCAATACCTACTATGCAATGAAGGTGTCTCCAAAAGAGTGTATCCCGCAGGCGCG 599
QY 679 CTTTCCAGCTCGCCCTCCCGCAGAGGGTCCCGAGGCTGCCAGGAGGAGGACCAAGCA 738
DB 600 CTTTCCAGCTCGCCCTCCACCCCGAGGACCCCGGCAGCTCTGAGGGCTGATCGACC 659
QY 739 GCTGCTGCCCTGGAGCGGGTGTACAGGAGATTGCCATCTCTGAAAGAGCTGGACCACT 798
DB 660 CAGGGGCGCCATTTAGCAGGCTGTACAGGAAATGCCATCTCTCAAGAGCTGGACCAACC 719
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DB 720 CAATGTGTGAAGCTGGTGGAGGCTCTGGATGACCCCAATGAGGACCACTGTGATCATGGT 779
QY 859 GTTTGACCTCTCGAAAGGGGCGCGTCAATGAAGTGCCTGTGCAAGAGCCCTCTCCGA 918
DB 780 GTTCGAATGTGTCAACCAAGGGCGGTGATGGAGTGGCCACCTCTCAACCACTCTCTGA 839
QY 919 GGAGCAAGCTGCTCTACTCTGCGGAGCGTCACTCTGGGCGCTCGAGTACTTGCACTGCA 978
DB 840 AGACCAGGCGCGTTTCTACTTCCAGGATCTGATCAAGGCGATCGAGTACTTACACTACCA 899
QY 979 GAAGATCTCCACAGGACATCAAGCCATCCAACTGCTCTCTGGGGGATGATGGGACAGT 1038
DB 900 GAAGATCATCCACCGTGACATCAAACTTCCAACTCTCTGTCGGAGAGATGGGACAT 959
QY 1039 GAAGATCCCGACTTTTGGCGTCAGCAACAGTTTGAAGGGAACAGCGCTCAGCTCTCCAG 1098
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QY 1099 CACGGCGGAAACCCAGCATTCATGGCCCCCGAGGCGCATTTCTGATTCGGGCGAGGTT 1158
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DB 1440 GGTGAAGCAATGATACGTAAACGCTCTTTGGGAACCAATTCGAGGGG- --AGCCGGCG 1496
QY 1579 GGAAGAGCGATCCATGCTGTCTCCAGGAAACCTACTGTGAAAGAGGGTTTGGTGAAGG 1638
DB 1497 GGAGGAACGCTCACTGTGAGCGCTGGAAACTTGTCTCACCAGAAACCAACCAAGGGAATG 1556
QY 1639 GGGCAAGAGCCAGAGCTCCCGG 1662
DB 1557 TGAGTCCCTGTGTGAGCTCAAGGG 1580
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Db	1440	GGTGAAGACCATGATACGTAAACGCTCCTTTGGGAACCCATTCGAGGGC--AGCCGGCG	1496
QY	1579	GGAGAGCGATCCATGCTCTGCTCCAGGAACCTACTGGTGAAGAAGGGTTTGGTGAAGG	1638
Db	1497	GGAGGAACGCTCACTGTACGGCTCGAATCTTGTCTCACCACCAACCAACCGGGAATG	1556
QY	1639	GGCAAGAGCCAGAGCTCCCGG	1662
Db	1557	TGAGTCCCTGTCTGAGCTCAAGG	1580

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 Job time : 1383 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: July 12, 2004, 04:53:05 ; Search time 1695 Seconds
 (without alignments)
 92.931 Million cell updates/sec

Title: US-10-690-617-2
 Perfect score: 2634
 Sequence: 1 MEGPAPVCCQDRAELVERV.....FEGGKSPELPGVQDEAAS 505

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 1279676 seqs, 31191243 residues 1279676

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Published Applications AA.*

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 2: /cgn2_6/ptodata/2/pubpaa/FCT_NEW_PUB.pep.*
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 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
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 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2634	100.0	505	13	US-10-135-689-2	Sequence 2, Appli
2	2634	100.0	505	16	US-10-690-617-2	Sequence 2, Appli
3	2626	99.7	505	12	US-10-333-314-19	Sequence 18, Appl
4	2611	99.1	505	12	US-10-092-900A-56	Sequence 56, Appl
5	2595	98.5	513	12	US-10-168-582-2	Sequence 2, Appli
6	2591	98.4	561	9	US-09-922-138-8	Sequence 8, Appli
7	2591	98.4	561	16	US-10-391-364-42	Sequence 42, Appl
8	2585	98.1	543	12	US-10-092-900A-58	Sequence 58, Appl
9	2560	97.2	503	12	US-10-092-900A-54	Sequence 54, Appl
10	2468	93.7	505	13	US-10-135-689-4	Sequence 4, Appli
11	2468	93.7	505	16	US-10-690-617-4	Sequence 4, Appli
12	1525.5	57.9	556	14	US-10-205-823-52	Sequence 52, Appl
13	1518.5	57.6	588	14	US-10-316-124-9	Sequence 9, Appli
14	1518.5	57.6	588	15	US-10-295-027-1355	Sequence 1355, Ap
15	1472.5	55.9	417	14	US-10-205-823-54	Sequence 54, Appl

16 1043 39.6 357 15 US-10-369-493-5728 Sequence 5728, Ap
 17 923 35.0 210 12 US-10-296-115-759 Sequence 759, App
 18 649.5 24.7 465 15 US-10-369-493-3141 Sequence 3141, Ap
 19 620 23.5 652 16 US-10-618-581-28 Sequence 28, Appl
 20 611 23.2 140 12 US-10-296-115-986 Sequence 986, App
 21 566 21.5 1142 15 US-10-369-493-1767 Sequence 1767, Ap
 22 546.5 20.7 426 12 US-10-618-581-26 Sequence 26, Appl
 23 546.5 20.7 426 12 US-10-425-114-50357 Sequence 50357, A
 24 541.5 20.6 332 12 US-10-425-114-71396 Sequence 71396, A
 25 535 20.3 256 12 US-09-964-956-72 Sequence 72, Appl
 26 535 20.3 256 12 US-10-042-865-83 Sequence 83, Appl
 27 535 20.3 256 12 US-10-029-020-183 Sequence 183, App
 28 535 20.3 256 12 US-10-072-012-799 Sequence 799, App
 29 535 20.3 256 12 US-10-072-012-856 Sequence 856, App
 30 535 20.3 256 12 US-10-072-012-876 Sequence 876, App
 31 535 20.3 256 12 US-10-072-012-882 Sequence 882, App
 32 535 20.3 256 16 US-10-055-569A-99 Sequence 99, Appl
 33 534 20.3 254 15 US-10-074-978A-150 Sequence 150, App
 34 534 20.3 256 10 US-09-863-776-40 Sequence 40, Appl
 35 528 20.0 255 12 US-10-087-684-98 Sequence 98, Appl
 36 528 20.0 255 12 US-10-218-779-98 Sequence 98, Appl
 37 527.5 20.0 426 16 US-10-437-963-162422 Sequence 162422,
 38 527 20.0 251 15 US-10-052-648A-41 Sequence 41, Appl
 39 526 20.0 250 10 US-09-976-782-31 Sequence 31, Appl
 40 526 20.0 252 15 US-10-074-978A-160 Sequence 160, App
 41 519 19.7 250 12 US-10-042-865-102 Sequence 102, App
 42 518.5 19.7 1408 16 US-10-618-581-29 Sequence 29, Appl
 43 507.5 19.3 560 15 US-10-369-493-21916 Sequence 21916, A
 44 504 19.1 256 10 US-09-823-187-96 Sequence 96, Appl
 45 496 18.8 234 15 US-10-231-913-266 Sequence 266, App

ALIGNMENTS

RESULT 1

US-10-135-689-2
 ; Sequence 2, Application US/10135689
 ; Publication No. US20020123121A1
 ; GENERAL INFORMATION:
 ; APPLICANT: WEI, Ming-Hui et al.
 ; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
 ; ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
 ; TITLE OF INVENTION: THEREOF
 ; FILE REFERENCE: CL000904DIV
 ; CURRENT APPLICATION NUMBER: US/10/135,689
 ; CURRENT FILING DATE: 2002-05-01
 ; PRIOR APPLICATION NUMBER: 60/247,031
 ; PRIOR FILING DATE: 2000-11-13
 ; PRIOR APPLICATION NUMBER: 09/729,995
 ; PRIOR FILING DATE: 2000-12-06
 ; NUMBER OF SEQ ID NOS: 4
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 2
 ; LENGTH: 505
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-135-689-2

Query Match 100.0%; Score 2634; DB 13; Length 505;
 Best Local Similarity 100.0%; Pred. No. 5.4e-205;
 Matches 505; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEGPAPVCCQDRAELVERVAIDVTHLEADGGPEPTRNGVDPVPPRARAASVIPGSTR 60
 |||||
 DB 1 MEGPAPVCCQDRAELVERVAIDVTHLEADGGPEPTRNGVDPVPPRARAASVIPGSTR 60
 |||||

QY 61 LLPAPSLARKLSLOERPAGSYLEAQAQPVATGPASHISPRAWRPTTISHHVAISDAE 120
 |||||
 DB 61 LLPAPSLARKLSLOERPAGSYLEAQAQPVATGPASHISPRAWRPTTISHHVAISDAE 120
 |||||

QY 121 DCVQLNQYKQSEITGKAYGVVRLAYNESDRHYAMKVLKSKLLKQYGFPRPPRGSQ 180
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Db 181 AAQGGPAKQLPLERVYQEIALLKLDHNVNKKLIEVLDDPAEDNLYLVFDLLRKGPVME 240
QY 241 VPCDKPSEBQARLYLRDVLGLYLEYLCQKIVHRDIKPSNLLGDDGHVKIADFGVSNQF 300
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Db 301 EGNDAQLSSTAGTAPAFMAPEAISDSQSGSKALDVWATGVTLYCFYVYKCPFIIDDFILA 360
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QY 421 EHCSCVVVEVTEGEVKNVRLIPSWTTVILVKSMRKRSFGNPFEPQARRERSMSAPGNL 480
Db 421 EHCSCVVVEVTEGEVKNVRLIPSWTTVILVKSMRKRSFGNPFEPQARRERSMSAPGNL 480
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; Sequence 2, Application US/10690617
; Publication No. US20040086926A1
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL000904DIV II
; CURRENT APPLICATION NUMBER: US/10/690,617
; CURRENT FILING DATE: 2003-10-23
; PRIOR APPLICATION NUMBER: 60/247,031
; PRIOR FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: 09/729,995
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 505
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-690-617-2

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Best Local Similarity 100.0%; Pred. No. 5.4e-205;
Matches 505; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 61 LLPARPSLSARKLSLOERPAGSYLEAQAGPYATGPASHISPAWRRTPTIESHHVAISDAE 120
QY 121 DCVOLNQYKLSQEIKGAGVVRVLAAYNESEDRHYAMKVLKKLLKQYGFPRPPRGSQ 180
Db 121 DCVOLNQYKLSQEIKGAGVVRVLAAYNESEDRHYAMKVLKKLLKQYGFPRPPRGSQ 180
QY 181 AAQGGPAKQLPLERVYQEIALLKLDHNVNKKLIEVLDDPAEDNLYLVFDLLRKGPVME 240
Db 181 AAQGGPAKQLPLERVYQEIALLKLDHNVNKKLIEVLDDPAEDNLYLVFDLLRKGPVME 240
QY 241 VPCDKPSEBQARLYLRDVLGLYLEYLCQKIVHRDIKPSNLLGDDGHVKIADFGVSNQF 300
```

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Db 241 VPCDKPSEBQARLYLRDVLGLYLEYLCQKIVHRDIKPSNLLGDDGHVKIADFGVSNQF 300
QY 301 EGNDAQLSSTAGTAPAFMAPEAISDSQSGSKALDVWATGVTLYCFYVYKCPFIIDDFILA 360
Db 301 EGNDAQLSSTAGTAPAFMAPEAISDSQSGSKALDVWATGVTLYCFYVYKCPFIIDDFILA 360
QY 361 LHRKIKNEPVVFPPEPISBELKDLILKMLDKNPETRIGVDPDIKLPWPVTKNGEELPSE 420
Db 361 LHRKIKNEPVVFPPEPISBELKDLILKMLDKNPETRIGVDPDIKLPWPVTKNGEELPSE 420
QY 421 EHCSCVVVEVTEGEVKNVRLIPSWTTVILVKSMRKRSFGNPFEPQARRERSMSAPGNL 480
Db 421 EHCSCVVVEVTEGEVKNVRLIPSWTTVILVKSMRKRSFGNPFEPQARRERSMSAPGNL 480
QY 481 LVKEGFEGGKSPELPGVQDEAAS 505
Db 481 LVKEGFEGGKSPELPGVQDEAAS 505

RESULT 3
US-10-333-314-19
; Sequence 19, Application US/10333314
; Publication No. US20030211093A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.; YUE, Henry
; APPLICANT: KHAN, Farrah A.; GURURAJAN, Rajagopal
; APPLICANT: HAPALIA, April J.A.; CHAWLA, Navinder K.
; APPLICANT: ARVIZO, Chandra S.; RAMKUMAR, Jayalaxmi
; APPLICANT: GANDHI, Ameena R.; POLICKY, Jennifer L.
; APPLICANT: BAUGHN, Mariah R.; TRIBOULEY, Catherine M.
; APPLICANT: THORNTON, Michael B.; BANDMAN, Olga
; APPLICANT: NGUYEN, Daniel B.; LU, Yan
; APPLICANT: BURFORD, Neil; LAL, Preeti G.
; APPLICANT: DING, Li; YAO, Monique G.
; APPLICANT: ELLIOTT, Vicki S.; RECIPON, Shirley A.
; APPLICANT: KEARNEY, Liam; LU, Dyung Aina M.
; APPLICANT: GREENWALD, Sara R.; TANG, Y. Tom
; APPLICANT: XU, Yuming; WALSH, Roderick T.
; APPLICANT: GIETZEN, Kimberly J.; YANG, Junming
; APPLICANT: JACKSON, Jennifer L.
; TITLE OF INVENTION: HUMAN KINASES
; FILE REFERENCE: FI-0162 USN
; CURRENT APPLICATION NUMBER: US/10/333,314
; CURRENT FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: PCT/US01/23092
; PRIOR FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/220,038
; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: US 60/222,112
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/222,831
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: US 60/224,729
; PRIOR FILING DATE: 2000-08-11
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PERL Program
; SEQ ID NO 19
; LENGTH: 505
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 2190612CD1
US-10-333-314-19

Query Match 99.7%; Score 2626; DB 12; Length 505;
Best Local Similarity 99.8%; Pred. No. 2.4e-204;
Matches 504; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MEGGPVCCQDPRAELVERVAADIVTHLEADGGPEPTRNGVDPPPRARAASVIPGSTSR 60
Db 1 MEGGPVCCQDPRAELVERVAADIVTHLEADGGPEPTRNGVDPPPRARAASVIPGSTSR 60
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QY 61 LLPARPSLSARKLSLOERPAGSYLEAQAQGYATGPASHISPRAWRPTTIESHHVAISDAE 120
DB 61 LLPARPSLSARKLSLOERPAGSYLEAQAQGYATGPASHISPRAWRPTTIESHHVAISDAE 120
QY 121 DCVOLNOYKLOSEIGKAGYGVRLAYNESEDRHYAMKVLKSKKLLKQYGFPRPPRGSO 180
DB 121 DCVOLNOYKLOSEIGKAGYGVRLAYNESEDRHYAMKVLKSKKLLKQYGFPRPPRGSO 180
QY 181 AAQGGPAKQLPLERVYQEIALLKLDHVNKKLIEVLDDPAEDNLVLFVDFLLRKGPNME 240
DB 181 AAQGGPAKQLPLERVYQEIALLKLDHVNKKLIEVLDDPAEDNLVLFVDFLLRKGPNME 240
QY 241 VPCDKPFSSEQARLYLRDVLGLYHLCQKI VHRDIKPSNLLGDDGHVKIADFGVSNQF 300
DB 241 VPCDKPFSSEQARLYLRDVLGLYHLCQKI VHRDIKPSNLLGDDGHVKIADFGVSNQF 300
QY 301 EGNDAQLSSTAGTPAPMAPEALSDSGSFGKALDVWATGVTLVCFVYKCPFDIDFILA 360
DB 301 EGNDAQLSSTAGTPAPMAPEALSDSGSFGKALDVWATGVTLVCFVYKCPFDIDFILA 360
QY 361 LHRKIKNEPVPFPEPEISEELKDLILKMLDKNPETRIGVDPDIKLPWYTKNGEPLPSE 420
DB 361 LHRKIKNEPVPFPEPEISEELKDLILKMLDKNPETRIGVDPDIKLPWYTKNGEPLPSE 420
QY 421 EHCSSVVEVTEBEVKNSVRLIPSWTTLVVKSMKRKSGFNGNPFEPQARREERSMAGPGL 480
DB 421 EHCSSVVEVTEBEVKNSVRLIPSWTTLVVKSMKRKSGFNGNPFEPQARREERSMAGPGL 480
QY 481 LVKEGFGEGGKSPELPGVQDEAAS 505
DB 481 LVKEGFGEGGKSPELPGVQDEAAS 505

RESULT 4
US-10-092-900A-56
; Sequence 56, Application US/10092900A
; Publication No. US20040043382A1
; GENERAL INFORMATION:
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Taupier Jr., Raymond J.
; APPLICANT: Pena, Carol E.A.
; APPLICANT: Li, Li
; APPLICANT: Zethusen, Bryan D.
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Ji, Weizhen
; APPLICANT: Gorman, Linda
; APPLICANT: Miller, Charles E.
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Patturajan, Meera
; APPLICANT: Gangolli, Esha A.
; APPLICANT: Vernet, Corine A.M.
; APPLICANT: Guo, Xiaojia Sashu
; APPLICANT: Tchernev, Velizar T.
; APPLICANT: Fernandes, Elma R.
; APPLICANT: Casman, Stacie J.
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Liu, Yi
; APPLICANT: Anderson, David W.
; APPLICANT: Spaderna, Steven K.
; APPLICANT: Catterton, Elina
; APPLICANT: Leite, Mario W.
; APPLICANT: Zhong, Haihong
; APPLICANT: Alsobrook, John P.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Burgess, Catherine E.
; TITLE OF INVENTION: No. US20040043382A1el Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-290C
; CURRENT APPLICATION NUMBER: US/10/092, 900A
; CURRENT FILING DATE: 2002-03-07

; PRIOR APPLICATION NUMBER: USSN 60/274,322
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: USSN 60/283,675
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: USSN 60/338,092
; PRIOR FILING DATE: 2001-12-03
; PRIOR APPLICATION NUMBER: USSN 60/274,281
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: USSN 60/274,191
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: USSN 60/325,681
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: USSN 60/304,354
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: USSN 60/279,995
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: USSN 60/294,899
; PRIOR FILING DATE: 2001-05-31
; PRIOR APPLICATION NUMBER: USSN 60/287,424
; PRIOR FILING DATE: 2001-04-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 768
; SEQ ID NO 56
; LENGTH: 505
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-092-900A-56

Query Match 99.1%; Score 2611; DB 12; Length 505;
Best Local Similarity 99.4%; Pred. No. 4e-203;
Matches 502; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MEGGPAVCCQDPRAELVERVAIDVTHLEADGGPEPTRNGVDPPPRARAASVIGSTSR 60
DB 1 MEGGPAVCCQDPRAELVERVAIDVTHLEADGGPEPTRNGVDPPPRARAASVIGSTSR 60
QY 61 LLPARPSLSARKLSLOERPAGSYLEAQAQGYATGPASHISPRAWRPTTIESHHVAISDAE 120
DB 61 LLPARPSLSARKLSLOERPAGSYLEAQAQGYATGPASHISPRAWRPTTIESHHVAISDAE 120
QY 121 DCVOLNOYKLOSEIGKAGYGVRLAYNESEDRHYAMKVLKSKKLLKQYGFPRPPRGSO 180
DB 121 DCVOLNOYKLOSEIGKAGYGVRLAYNESEDRHYAMKVLKSKKLLKQYGFPRPPRGSO 180
QY 181 AAQGGPAKQLPLERVYQEIALLKLDHVNKKLIEVLDDPAEDNLVLFVDFLLRKGPNME 240
DB 181 AAQGGPAKQLPLERVYQEIALLKLDHVNKKLIEVLDDPAEDNLVLFVDFLLRKGPNME 240
QY 241 VPCDKPFSSEQARLYLRDVLGLYHLCQKI VHRDIKPSNLLGDDGHVKIADFGVSNQF 300
DB 241 VPCDKPFSSEQARLYLRDVLGLYHLCQKI VHRDIKPSNLLGDDGHVKIADFGVSNQF 300
QY 301 EGNDAQLSSTAGTPAPMAPEALSDSGSFGKALDVWATGVTLVCFVYKCPFDIDFILA 360
DB 301 EGNDAQLSSTAGTPAPMAPEALSDSGSFGKALDVWATGVTLVCFVYKCPFDIDFILA 360
QY 361 LHRKIKNEPVPFPEPEISEELKDLILKMLDKNPETRIGVDPDIKLPWYTKNGEPLPSE 420
DB 361 LHRKIKNEPVPFPEPEISEELKDLILKMLDKNPETRIGVDPDIKLPWYTKNGEPLPSE 420
QY 421 EHCSSVVEVTEBEVKNSVRLIPSWTTLVVKSMKRKSGFNGNPFEPQARREERSMAGPGL 480
DB 421 EHCSSVVEVTEBEVKNSVRLIPSWTTLVVKSMKRKSGFNGNPFEPQARREERSMAGPGL 480
QY 481 LVKEGFGEGGKSPELPGVQDEAAS 505
DB 481 LVKEGFGEGGKSPELPGVQDEAAS 505

RESULT 5
US-10-168-582-2
; Sequence 2, Application US/10168582
; Publication No. US20040058426A1

```
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: YANG, Junming
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: BURFORD, Neil
; APPLICANT: AU-YOUNG, Janice
; APPLICANT: LU, Dyung Aina M.
; APPLICANT: REDDY, Roopa
; APPLICANT: YUE, Henry
; APPLICANT: YAO, Monique G.
; APPLICANT: LAL, Preeti
; APPLICANT: KAHN, Farrah A.
; TITLE OF INVENTION: HUMAN KINASES
; FILE REFERENCE: PI-0002 PCT
; CURRENT APPLICATION NUMBER: US/10/168,582
; CURRENT FILING DATE: 2002-06-20
; PRIOR APPLICATION NUMBER: 60/172,066; 60/176,107; 60/176,107; 60/177,731
; PRIOR FILING DATE: 1999-12-23; 2000-01-14; 2000-01-14; 2000-01-21
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PERL Program
; SEQ ID NO 2
; LENGTH: 513
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20040058426A1 2041716CD1
US-10-168-582-2

Query Match      98.5%; Score 2595; DB 12; Length 513;
Best Local Similarity 97.9%; Pred. No. 8.1e-202;
Matches 503; Conservative 0; Mismatches 1; Indels 10; Gaps 2;

Qy      1 MEGGPAVCCDDPRAELVERVAADVTTHLEADGGPEPTRNGVDPPPPARAASVIPGSTSR 60
Db      1 MEGGPAVCCDDPRAELVERVAADVTTHLEADGGPEPTRNGVDPPPPARAASVIPGSTSR 60

Qy      61 LLPARPSLSARKLSLOERPAAGSYLEAQAQPYATGPASHISPRAWRRPTTIESHHVAISDAE 120
Db      61 LLPARPSLSARKLSLOERPAAGSYLEAQAQPYATGPASHISPRAWRRPTTIESHHVAISDAE 120

Qy      121 DCVQLNQYKLOSETGK-----GAYGVVRLAYNESDRHYAMKVLKSKLLKQYGF 171
Db      121 DCVQLNQYKLOSETGKVLGLTDAYLQAGAYGVVRLAYNESDRHYAMKVLKSKLLKQYGF 180

Qy      172 RPPPPGSAQAQGPAPKQLPLERVYQEIALLKLDHNVVVKLIEVLDDPAEDNLVLF 231
Db      181 RPPPPGSAQAQGPAPKQLPLERVYQEIALLKLDHNVVVKLIEVLDDPAEDNLVLF-D 239

Qy      232 LLRKGVPWVPCDKPFSEQARLYLVDVILGLEYLHCQKIVHRDIKPSNLLLGDDGHVKI 291
Db      240 LLRKGVPWVPCDKPFSEQARLYLVDVILGLEYLHCQKIVHRDIKPSNLLLGDDGHVKI 299

Qy      292 ADFGVSNQFEGNDAQLSSTAGTAPFAPEAISDSQSFSKALDVWATGVTLYCFVYKGC 351
Db      300 ADFGVSNQFEGNDAQLSSTAGTAPFAPEAISDSQSFSKALDVWATGVTLYCFVYKGC 359

Qy      352 PFIDDFILALHRLKNEPVFPPEPEISEELKDLILKMLDKNPETRGVDDIKLHPWTK 411
Db      360 PFIDDFILALHRLKNEPVFPPEPEISEELKDLILKMLDKNPETRGVDDIKLHPWTK 419

Qy      412 NGEPLPSEEHCSVWVTEGEVKNVRLIPSWTTVILVKSMLRKSGFNPFPQARRE 471
Db      420 NGEPLPSEEHCSVWVTEGEVKNVRLIPSWTTVILVKSMLRKSGFNPFPQARRE 479

Qy      472 RMSAPGNLLVKEFGGKSPPLPGVQEDAAAS 505
Db      480 RMSAPGNLLVKEFGGKSPPLPGVQEDAAAS 513

RESULT 6
US-09-922-138-8
; Sequence 8, Application US/09922138

; Patent No. US20020061574A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Meyers, Rachel
; APPLICANT: Silos-Santiago, Immaculada
; TITLE OF INVENTION: 16658, 14223, AND 16002, NOVEL HUMAN
; TITLE OF INVENTION: KINASES AND USES THEREFOR
; FILE REFERENCE: 38155-20030.00
; CURRENT APPLICATION NUMBER: US/09/922,138
; CURRENT FILING DATE: 2001-11-28
; PRIOR APPLICATION NUMBER: US 60/229,299
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 561
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-922-138-8

Query Match      98.4%; Score 2591; DB 9; Length 561;
Best Local Similarity 99.6%; Pred. No. 1.9e-201;
Matches 497; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 MEGGPAVCCDDPRAELVERVAADVTTHLEADGGPEPTRNGVDPPPPARAASVIPGSTSR 60
Db      1 MEGGPAVCCDDPRAELVERVAADVTTHLEADGGPEPTRNGVDPPPPARAASVIPGSTSR 60

Qy      61 LLPARPSLSARKLSLOERPAAGSYLEAQAQPYATGPASHISPRAWRRPTTIESHHVAISDAE 120
Db      61 LLPARPSLSARKLSLOERPAAGSYLEAQAQPYATGPASHISPRAWRRPTTIESHHVAISDAE 120

Qy      121 DCVQLNQYKLOSETGKAGYGVVRLAYNESDRHYAMKVLKSKLLKQYGP 180
Db      121 DCVQLNQYKLOSETGKAGYGVVRLAYNESDRHYAMKVLKSKLLKQYGP 180

Qy      181 AAGGPAKQLPLERVYQEIALLKLDHNVVVKLIEVLDDPAEDNLVLF 240
Db      181 AAGGPAKQLPLERVYQEIALLKLDHNVVVKLIEVLDDPAEDNLVLF 240

Qy      241 VPCDKPFSEQARLYLVDVILGLEYLHCQKIVHRDIKPSNLLLGDDGHVKIADFGVSNQF 300
Db      241 VPCDKPFSEQARLYLVDVILGLEYLHCQKIVHRDIKPSNLLLGDDGHVKIADFGVSNQF 300

Qy      301 EGNDAQLSSTAGTAPFAPEAISDSQSFSKALDVWATGVTLYCFVYKCPFI 360
Db      301 EGNDAQLSSTAGTAPFAPEAISDSQSFSKALDVWATGVTLYCFVYKCPFI 360

Qy      361 LHRKIKNEPVFPPEPEISEELKDLILKMLDKNPETRGVDDIKLHPWTKNGEPLPSE 420
Db      361 LHRKIKNEPVFPPEPEISEELKDLILKMLDKNPETRGVDDIKLHPWTKNGEPLPSE 420

Qy      421 EHCSSVVEVTEGEVKNVRLIPSWTTVILVKSMLRKSGFNPFPQARRE 480
Db      421 EHCSSVVEVTEGEVKNVRLIPSWTTVILVKSMLRKSGFNPFPQARRE 480

Qy      481 LVKEGFGGKSPPLPGVQ 499
Db      481 LVKEGFGGKSPPLPGVQ 499

RESULT 7
US-10-391-364-42
; Sequence 42, Application US/10391364
; Publication No. US20040121349A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Meyers, Rachel E.
; APPLICANT: Carroll, Joseph M.
; APPLICANT: Cook, William James
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: Weich, Nadine S.
; APPLICANT: Bandaru, Rajasekhar
```


1 TITLE OF INVENTION: NOVEL 27877, 18080, 14081, 32140, 50352,
2 TITLE OF INVENTION: 16558, 14223, 16002, 50566, 65552 AND 65577 MOLECULES AND
3 TITLE OF INVENTION: US95 THEREFOR
4 FILE REFERENCE: MPI03-0190NMIM
5 CURRENT APPLICATION NUMBER: US/10/391,364
6 CURRENT FILING DATE: 2003-03-18
7 PRIOR FILING DATE: US 09/950,370
8 PRIOR FILING DATE: 2001-09-10
9 PRIOR APPLICATION NUMBER: US 60/231,084
10 PRIOR FILING DATE: 2000-09-08
11 PRIOR APPLICATION NUMBER: US 10/294,039
12 PRIOR FILING DATE: 2002-11-13
13 PRIOR APPLICATION NUMBER: US 60/338,587
14 PRIOR FILING DATE: 2001-11-13
15 PRIOR APPLICATION NUMBER: US 10/266,035
16 PRIOR FILING DATE: 2002-10-07
17 PRIOR APPLICATION NUMBER: US 60/328,198
18 PRIOR FILING DATE: 2001-10-09
19 PRIOR APPLICATION NUMBER: US 09/717,926
20 PRIOR FILING DATE: 2000-11-21
21 PRIOR APPLICATION NUMBER: US 60/214,707
22 PRIOR FILING DATE: 2000-06-27
23 PRIOR APPLICATION NUMBER: US 10/268,036
24 PRIOR FILING DATE: 2002-10-09
25 PRIOR APPLICATION NUMBER: US 60/327,820
26 PRIOR FILING DATE: 2001-10-09
27 Remaining Prior Application data removed - See File Wrapper or PALM.
28 NUMBER OF SEQ ID NOS: 93
29 SOFTWARE: FastSeq for Windows Version 4.0
30 SEQ ID NO 42
31 LENGTH: 561
32 TYPE: PRT
33 ORGANISM: Homo sapiens
34 US-10-391-364-42

Query Match 98.4%; Score 2591; DB 16; Length 561;
Best Local Similarity 99.6%; Pred. No. 1.9e-201;
Matches 497; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 MEGGPAVCCDPAELVERVAIDVTHLEADGGPEPTRNGVDPPRARAASVIFGSTR 60
DB 1 MEGGPAVCCDPAELVERVAIDVTHLEADGGPEPTRNGVDPPRARAASVIFGSTR 60
QY 61 LPARPSLSARSLQERPAAGSYLAQAGPYATGASHISPAWRPTTIESHHVAISDAE 120
DB 61 LPARPSLSARSLQERPAAGSYLAQAGPYATGASHISPAWRPTTIESHHVAISDAE 120
QY 121 DCVQLNQYKLSQEIKGAGYGVVRLAYNESEDRHYAMKVLKKLLKQYGFPRPPRGSQ 180
DB 121 DCVQLNQYKLSQEIKGAGYGVVRLAYNESEDRHYAMKVLKKLLKQYGFPRPPRGSQ 180
QY 181 AAQGPAPKQLPLERYQEIALLKLDHVNKKLIEVLDPAEDNLVFDLLRKGPMVE 240
DB 181 AAQGPAPKQLPLERYQEIALLKLDHVNKKLIEVLDPAEDNLVFDLLRKGPMVE 240
QY 241 VPCDKPFSEEQARLYRDLVILGLEVHCQKIVHRDIPKSNLLGDDGHVKIADFGVSNQF 300
DB 241 VPCDKPFSEEQARLYRDLVILGLEVHCQKIVHRDIPKSNLLGDDGHVKIADFGVSNQF 300
QY 301 EGNDALSLSTAGTAFMAPEAISDSGQSFSGKALDVWATGVTLYCFVYKCPFFIDDFILA 360
DB 301 EGNDALSLSTAGTAFMAPEAISDSGQSFSGKALDVWATGVTLYCFVYKCPFFIDDFILA 360
QY 361 LHRKIKNEPVVFPPEPTESEELKOLILKMLDKNPETRIGVDPDKLHPWVTNKGEPFLPSE 420
DB 361 LHRKIKNEPVVFPPEPTESEELKOLILKMLDKNPETRIGVDPDKLHPWVTNKGEPFLPSE 420
QY 421 EHCSCVWTEGEVKNVRLIPSWTIVLVKMLKRSFGNPFEPQARREERSMAPGNL 480
DB 421 EHCSCVWTEGEVKNVRLIPSWTIVLVKMLKRSFGNPFEPQARREERSMAPGNL 480
QY 481 LVKEGFGEGKSPPELPGVQ 499
DB 481 LVKEGFGEGKSPPELPGVQ 499

Db 481 LVKEGFGEGKSPPELPGVQ 499
RESULT 8
US-10-092-900A-58
1 Sequence 58, Application US/10092900A
2 Publication No. US20040043382A1
3 GENERAL INFORMATION:
4 APPLICANT: Padigar, Muralidhara
5 APPLICANT: Spytek, Kimberly A.
6 APPLICANT: Shenoy, Suresh G.
7 APPLICANT: Taupier Jr., Raymond J.
8 APPLICANT: Pena, Carol E.A.
9 APPLICANT: Li, Li
10 APPLICANT: Zerhusen, Bryan D.
11 APPLICANT: Gusev, Vladimir Y.
12 APPLICANT: Ji, Weizhen
13 APPLICANT: Gorman, Linda
14 APPLICANT: Miller, Charles E.
15 APPLICANT: Kekuda, Ramesh
16 APPLICANT: Patturajan, Meera
17 APPLICANT: Gangolli, Esha A.
18 APPLICANT: Vernet, Corine A.M.
19 APPLICANT: Guo, Xiaojia Sasha
20 APPLICANT: Tchernev, Velizar T.
21 APPLICANT: Fernandes, Elma R.
22 APPLICANT: Casman, Stacie J.
23 APPLICANT: Malvankar, Uriel M.
24 APPLICANT: Gerlach, Valerie
25 APPLICANT: Liu, Yi
26 APPLICANT: Anderson, David W.
27 APPLICANT: Spaderna, Steven K.
28 APPLICANT: Catterton, Elina
29 APPLICANT: Leite, Mario W.
30 APPLICANT: Zhong, Haihong
31 APPLICANT: Alsobrook, John P.
32 APPLICANT: Lepley, Denise M.
33 APPLICANT: Rieger, Daniel K.
34 APPLICANT: Burgess, Catherine E.
35 TITLE OF INVENTION: No. US20040043382A1el Proteins and Nucleic Acids Encoding Same
36 FILE REFERENCE: 21402-290C
37 CURRENT APPLICATION NUMBER: US/10/092,900A
38 CURRENT FILING DATE: 2002-03-07
39 PRIOR APPLICATION NUMBER: USSN 60/274,322
40 PRIOR FILING DATE: 2001-03-08
41 PRIOR APPLICATION NUMBER: USSN 60/283,675
42 PRIOR FILING DATE: 2001-04-13
43 PRIOR APPLICATION NUMBER: USSN 60/338,092
44 PRIOR FILING DATE: 2001-12-03
45 PRIOR APPLICATION NUMBER: USSN 60/274,281
46 PRIOR FILING DATE: 2001-03-08
47 PRIOR APPLICATION NUMBER: USSN 60/274,191
48 PRIOR FILING DATE: 2001-03-08
49 PRIOR APPLICATION NUMBER: USSN 60/325,681
50 PRIOR FILING DATE: 2001-09-27
51 PRIOR APPLICATION NUMBER: USSN 60/304,354
52 PRIOR FILING DATE: 2001-07-10
53 PRIOR APPLICATION NUMBER: USSN 60/279,995
54 PRIOR FILING DATE: 2001-03-30
55 PRIOR APPLICATION NUMBER: USSN 60/294,899
56 PRIOR FILING DATE: 2001-05-31
57 PRIOR APPLICATION NUMBER: USSN 60/287,424
58 PRIOR FILING DATE: 2001-04-30
59 Remaining Prior Application data removed - See File Wrapper or PALM.
60 NUMBER OF SEQ ID NOS: 768
61 SEQ ID NO 58
62 LENGTH: 543
63 TYPE: PRT
64 ORGANISM: Homo sapiens
65 US-10-092-900A-58

Query Match 98.1%; Score 2585; DB 12; Length 543;
Best Local Similarity 92.4%; Pred. No. 5.7e-201;

QY 481 LVKEGFGGKSPFLPGVQDEAAS 505
|
Db 479 LVKEGFGGKSPFLPGVQDEAAS 503

RESULT 10
US-10-135-689-4
; Sequence 4, Application US/10135689
; Publication No. US20020123121A1
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: CL000904DIV II
; CURRENT FILING DATE: 2002-05-01
; PRIOR APPLICATION NUMBER: 60/247,031
; PRIOR FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: 09/729,995
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 505
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-135-689-4

Query Match 93.7%; Score 2468; DB 13; Length 505;
Best Local Similarity 93.5%; Pred. No. 1.6e-191;
Matches 472; Conservative 11; Mismatches 22; Indels 0; Gaps 0;

QY 1 MEGGPAVCCQDPRAELVERVAIDVTHLEADGGPEPTRNGVDPPPRARAASVPGSTGR 60
||
Db 1 MERSPAVCCQDPRAELVERVAISVAHLEAEAGPEPAGNGVDPPPRARAASVPGSAR 60

QY 61 LIPAPSLSARKLSQERPAAGVYLAQAGPYATGPASHISPRAWRPTTIESHHVAISDAE 120
||
Db 61 PTPVRPSLSARKFSQERPAAGVYLAQAGPYATGPASHISPRAWRPTTIESHHVAISDTE 120

QY 121 DCVQLNOYKLOSEIGKAGGVVRLAYNESEDRHYAMKVLKKKLLKQYGFPRPPRGSQ 180
||
Db 121 DCVQLNOYKLOSEIGKAGGVVRLAYNEREDRHYAMKVLKKKLLKQYGFPRPPRGSQ 180

QY 181 AAQGGPAKQLPLERVYQEIAILKKLDHVVVVKLIEVLDDPAEDNLVLFVLLRKGPMVE 240
||
Db 181 APQGGPAKQLPLERVYQEIAILKKLDHVVVVKLIEVLDDPAEDNLVLFVLLRKGPMVE 240

QY 241 VPCDPFSEQARLYLRDVLGLVYHCOKIVHRDIKPSNLLGGDGHVKIADFGVSNQF 300
||
Db 241 VPCDPFPEEQARLYLRDILGLVYHCOKIVHRDIKPSNLLGGDGHVKIADFGVSNQF 300

QY 301 EGNDAQLSSTAGTAPFMAPEATSDGQSFSGKALDVWATGVTLYCFVYKCPFIIDFILA 360
||
Db 301 EGNDAQLSSTAGTAPFMAPEATSDGQSFSGKALDVWATGVTLYCFVYKCPFIIDFILA 360

QY 361 LHRKIKNEAVVPFPEVSEELKDILKMLDKNPETRIGVPDIKLPWTKNGEPLPSE 420
||
Db 361 LHRKIKNEAVVPFPEVSEELKDILKMLDKNPETRIGVSDIKLPWTKNGEPLPSE 420

QY 421 EHCSEVVEVTEEVKNSVRLIPSWTTVILVKMLKRKSGFNGPFEQARREERMSAPGNL 480
||
Db 421 EHCSEVVEVTEEVKNSVRLIPSWTTVILVKMLKRKSGFNGPFEQARREERMSAPGNL 480

QY 481 LVKEGFGGKSPFLPGVQDEAAS 505
|
Db 481 LVKEGFGGKSPFLPGVQDEAAS 505

RESULT 11
US-10-690-617-4

; Sequence 4, Application US/10690617
; Publication No. US20040086926A1
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: CL000904DIV II
; CURRENT FILING DATE: 2003-10-23
; PRIOR APPLICATION NUMBER: 60/247,031
; PRIOR FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: 09/729,995
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 505
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-690-617-4

Query Match 93.7%; Score 2468; DB 16; Length 505;
Best Local Similarity 93.5%; Pred. No. 1.6e-191;
Matches 472; Conservative 11; Mismatches 22; Indels 0; Gaps 0;

QY 1 MEGGPAVCCQDPRAELVERVAIDVTHLEADGGPEPTRNGVDPPPRARAASVPGSTGR 60
||
Db 1 MERSPAVCCQDPRAELVERVAISVAHLEAEAGPEPAGNGVDPPPRARAASVPGSAR 60

QY 61 LIPAPSLSARKLSQERPAAGVYLAQAGPYATGPASHISPRAWRPTTIESHHVAISDAE 120
||
Db 61 PTPVRPSLSARKFSQERPAAGVYLAQAGPYATGPASHISPRAWRPTTIESHHVAISDTE 120

QY 121 DCVQLNOYKLOSEIGKAGGVVRLAYNESEDRHYAMKVLKKKLLKQYGFPRPPRGSQ 180
||
Db 121 DCVQLNOYKLOSEIGKAGGVVRLAYNEREDRHYAMKVLKKKLLKQYGFPRPPRGSQ 180

QY 181 AAQGGPAKQLPLERVYQEIAILKKLDHVVVVKLIEVLDDPAEDNLVLFVLLRKGPMVE 240
||
Db 181 APQGGPAKQLPLERVYQEIAILKKLDHVVVVKLIEVLDDPAEDNLVLFVLLRKGPMVE 240

QY 241 VPCDPFSEQARLYLRDVLGLVYHCOKIVHRDIKPSNLLGGDGHVKIADFGVSNQF 300
||
Db 241 VPCDPFPEEQARLYLRDILGLVYHCOKIVHRDIKPSNLLGGDGHVKIADFGVSNQF 300

QY 301 EGNDAQLSSTAGTAPFMAPEATSDGQSFSGKALDVWATGVTLYCFVYKCPFIIDFILA 360
||
Db 301 EGNDAQLSSTAGTAPFMAPEATSDGQSFSGKALDVWATGVTLYCFVYKCPFIIDFILA 360

QY 361 LHRKIKNEAVVPFPEVSEELKDILKMLDKNPETRIGVPDIKLPWTKNGEPLPSE 420
||
Db 361 LHRKIKNEAVVPFPEVSEELKDILKMLDKNPETRIGVSDIKLPWTKNGEPLPSE 420

QY 421 EHCSEVVEVTEEVKNSVRLIPSWTTVILVKMLKRKSGFNGPFEQARREERMSAPGNL 480
||
Db 421 EHCSEVVEVTEEVKNSVRLIPSWTTVILVKMLKRKSGFNGPFEQARREERMSAPGNL 480

QY 481 LVKEGFGGKSPFLPGVQDEAAS 505
|
Db 481 LVKEGFGGKSPFLPGVQDEAAS 505

RESULT 12
US-10-205-823-52
; Sequence 52, Application US/10205823
; Publication No. US20030108963A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Endege, Wilson O.
; APPLICANT: Gannavarapu, Manjula
; APPLICANT: Gorbatcheva, Bella

; APPLICANT: Hoersch, Sebastian
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Wonsey, Angela M.
; APPLICANT: Glatt, Karen
; APPLICANT: Zhao, Xumei
; APPLICANT: Anderson, Dustin
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF PROSTATE CANCER
; FILE REFERENCE: MRI-044
; CURRENT APPLICATION NUMBER: US/10/205,823
; CURRENT FILING DATE: 2002-07-25
; PRIOR APPLICATION NUMBER: 60/307,982
; PRIOR FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: 60/314,356
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/325,020
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 60/341,746
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: 60/362,158
; PRIOR FILING DATE: 2002-03-05
; NUMBER OF SEQ ID NOS: 455
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 52
; LENGTH: 556
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-205-823-52

Query Match 57.9%; Score 1525.5; DB 14; Length 556;
Best Local Similarity 62.0%; Pred. No. 5.5e-115; Indels 31; Gaps 5;
Matches 299; Conservative 77; Mismatches 75; Indels 31; Gaps 5;
Qy 30 EADGGPEPTRNGVDPPPPARAASVPGSTSLRLPAREPSLSARKLSLOER-----PAGSYL 84
Db 75 EADQGEVP-----LDSSGSQ---ARPHLSGRKLSLQERSQGGGLAAGGSL 115
Qy 85 EAQAG-----PYATGPASHISPRAWRRPTIESHHVAISDAEDCVQLNOYKLSQSEIGKA 138
Db 116 DMNGRCICPSLPYSPVSSPQSPRLPRPTVESHHVSIITGMQDCVQLNQYTLKDEIGKGS 175
Qy 139 YGVVRLAYNESEDRHYAMKVLKLLKQYGFRRPPRPGSGAAQGGPAAKQLLPLERYQ 198
Db 176 YGVVRLAYNENDNYAMKVLKLLKQYGFRRPPRPGSGAAQGGPAAKQLLPLERYQ 235
Qy 199 EAILKXLDHNVVVKLIEVLDDPAEDNLVYFLLRKGPMVEVPCDKPFSEQARLYLRD 258
Db 236 EAILKXLDHNVVVKLIEVLDDPAEDNLVYFLLRKGPMVEVPCDKPFSEQARLYLRD 295
Qy 259 VILGLEVYLHCQKIVHRDIKPSNLLGDDGHVKIADFGVSNQFEGNDALSLSTAGTAPMA 318
Db 296 LIKGIEYLYHQKIHHRDIKPSNLLGDDGHVKIADFGVSNQFEGNDALSLSTAGTAPMA 355
Qy 319 PEALSDSGQSGKALDVWATGVTLYCFVYKCPFIIDDFILALHRKIKNEPWPPEPEI 378
Db 356 PESLSETRKIFSGKALDVWATGVTLYCFVYKCPFIIDDFILALHRKIKNEPWPPEPEI 415
Qy 379 SEELKDLILKMLDKNPETRIQVDPDKLHPWVTKNGEPLPSEEBHCHSVVEVTEGEVKNV 438
Db 416 AEDLKDLITRMLDKNPESRIWVPEIKLHPWVTRHGAEPLPSEEDENCTIVTEVEVENSV 475
Qy 439 RLIPSWTIVLVKMLKRSFGNPEPQARREERSMSPAGNLLVKEGEGGKSPPLPGV 498
Db 476 KHIPSLATVILVKTMRKRSFGNPEPQARREERSMSPAGNLLVKEGEGGKSPPLPGV 534
Qy 499 QE 500
Db 535 KK 536

RESULT 13
US-10-316-124-9

; Sequence 9, Application US/10316124
; Publication No. US20030152574A1
; GENERAL INFORMATION:
; APPLICANT: Logan, Thomas Joseph
; APPLICANT: Chun, Miyoung
; TITLE OF INVENTION: METHODS AND COMPOSITIONS TO TREAT
; TITLE OF INVENTION: CARDIOVASCULAR DISEASE USING 1419, 58765, AND 2210
; FILE REFERENCE: WPI01-291P1RM
; CURRENT APPLICATION NUMBER: US/10/316,124
; CURRENT FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: 60/339,995
; PRIOR FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 588
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-316-124-9

Query Match 57.6%; Score 1518.5; DB 14; Length 588;
Best Local Similarity 63.3%; Pred. No. 2.2e-114; Indels 31; Gaps 5;
Matches 295; Conservative 75; Mismatches 65; Indels 31; Gaps 5;
Qy 30 EADGGPEPTRNGVDPPPPARAASVPGSTSLRLPAREPSLSARKLSLOER-----PAGSYL 84
Db 75 EADQGEVP-----LDSSGSQ---ARPHLSGRKLSLQERSQGGGLAAGGSL 115
Qy 85 EAQAG-----PYATGPASHISPRAWRRPTIESHHVAISDAEDCVQLNOYKLSQSEIGKA 138
Db 116 DMNGRCICPSLPYSPVSSPQSPRLPRPTVESHHVSIITGMQDCVQLNQYTLKDEIGKGS 175
Qy 139 YGVVRLAYNESEDRHYAMKVLKLLKQYGFRRPPRPGSGAAQGGPAAKQLLPLERYQ 198
Db 176 YGVVRLAYNENDNYAMKVLKLLKQYGFRRPPRPGSGAAQGGPAAKQLLPLERYQ 235
Qy 199 EAILKXLDHNVVVKLIEVLDDPAEDNLVYFLLRKGPMVEVPCDKPFSEQARLYLRD 258
Db 236 EAILKXLDHNVVVKLIEVLDDPAEDNLVYFLLRKGPMVEVPCDKPFSEQARLYLRD 295
Qy 259 VILGLEVYLHCQKIVHRDIKPSNLLGDDGHVKIADFGVSNQFEGNDALSLSTAGTAPMA 318
Db 296 LIKGIEYLYHQKIHHRDIKPSNLLGDDGHVKIADFGVSNQFEGNDALSLSTAGTAPMA 355
Qy 319 PEALSDSGQSGKALDVWATGVTLYCFVYKCPFIIDDFILALHRKIKNEPWPPEPEI 378
Db 356 PESLSETRKIFSGKALDVWATGVTLYCFVYKCPFIIDDFILALHRKIKNEPWPPEPEI 415
Qy 379 SEELKDLILKMLDKNPETRIQVDPDKLHPWVTKNGEPLPSEEBHCHSVVEVTEGEVKNV 438
Db 416 AEDLKDLITRMLDKNPESRIWVPEIKLHPWVTRHGAEPLPSEEDENCTIVTEVEVENSV 475
Qy 439 RLIPSWTIVLVKMLKRSFGNPEPQARREERSMSPAGNLLVKE 484
Db 476 KHIPSLATVILVKTMRKRSFGNPEPQARREERSMSPAGNLLTKK 520

RESULT 14
US-10-295-027-1355
; Sequence 1355, Application US/10295027
; Publication No. US2003023350A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glynn, Richard
; APPLICANT: Hevezi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and

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; TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
; FILE REFERENCE: 018501-012500US
; CURRENT APPLICATION NUMBER: US/10/295,027
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 09/663,733
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/335,394
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/332,464
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/334,393
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/340,376
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/347,211
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/347,349
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/355,250
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/356,714
; PRIOR FILING DATE: 2002-02-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1355
; LENGTH: 588
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-295-027-1355
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Query Match      57.6%; Score 1518.5; DB 15; Length 588;
Best Local Similarity 63.3%; Pred. No. 2.2e-114;
Matches 295; Conservative 75; Mismatches 65; Indels 31; Gaps 5;

QY 30 EADGGPEPTRGVDPPPRARAASVTPGTSRLLPARPSLSARKLSIQER-----PAGSYL 84
DB 75 EADGGPEPTRGVDPPPRARAASVTPGTSRLLPARPSLSARKLSIQER-----PAGSYL 84
QY 85 EAQAG-----PVATGPASHISPRAWRRPTTISHHVAISDAEDCVOLNQYKLGSEIGKGA 138
DB 116 DWNGRCICPSLPYSPVSSQSSPRLPRPTVSHHVSITGMQDCVOLNQYTLKDEIGKGS 175
QY 139 YGVVRLAYNESDRHYAMKVLKSKKLLKQYGFPRPPRPGSQAAQGGPAKQLLPLERVVYQ 198
DB 176 YGVVRLAYNESDRHYAMKVLKSKKLLKQYGFPRPPRPGSQAAQGGPAKQLLPLERVVYQ 235
QY 199 EIALKLDHNVVVKLIEVLDPAEDNLYLVFDLRLKGPVMEVPCDKPFSEEQARLYLRD 258
DB 236 EIALKLDHNVVVKLIEVLDPAEDNLYLVFDLRLKGPVMEVPCDKPFSEEQARLYLRD 295
QY 259 VILGLEYLHCOKI VHRDIKPSNLLIGDDGHVKIADFGVSNQEPGNDALSSTAGTPAFMA 318
DB 296 LKGEYLYHYQKLIHRDIKPSNLLIGDDGHVKIADFGVSNQEPGNDALSSTAGTPAFMA 355
QY 319 PEATSDSQSGSKALDVMATGTYLCFYVYKCPFDIDDFILALHRRKIKNEPVVFPPEPEI 378
DB 356 PESLSETRKIFSGKALDVMATGTYLCFYVYKCPFDIDDFILALHRRKIKNEPVVFPPEPEI 415
QY 379 SEELKDLILKMDKNPETRIGVDPDKLHPWTKNGEELPLPSSEHCVSVVVTEGVKNSV 438
DB 416 AEDLKDLITRMLDKNPESRIVVPEIKLHPWTRHGAELPLPSDENCTLVEVTEEVENS 475
QY 439 RLIPSWTTVILVKMLRKESFGNPPEQARRREERSMSAPGNLLVKE 484
DB 476 KHIPSLATVILVKTMIRKRSFGNPPE-GSRREERSLSAPGNLLTKK 520
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RESULT 15
US-10-205-823-54
; Sequence 54, Application US/10205823
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; Publication No. US20030108963A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Endege, Wilson O.
; APPLICANT: Gannavarapu, Manjula
; APPLICANT: Gorbacheva, Bella
; APPLICANT: Hoersch, Sebastian
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Wansley, Angela M.
; APPLICANT: Glatt, Karen
; APPLICANT: Zhao, Xumel
; APPLICANT: Anderson, Dustin
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF PROSTATE CANCER
; FILE REFERENCE: MRI-044
; CURRENT APPLICATION NUMBER: US/10/205,823
; CURRENT FILING DATE: 2002-07-25
; PRIOR APPLICATION NUMBER: 60/307,982
; PRIOR FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: 60/314,356
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/325,020
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 60/341,746
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: 60/362,158
; PRIOR FILING DATE: 2002-03-05
; NUMBER OF SEQ ID NOS: 455
; SOFTWARE: FastSeq For Windows Version 4.0
; SEQ ID NO 54
; LENGTH: 417
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-205-823-54
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Query Match      55.9%; Score 1472.5; DB 14; Length 417;
Best Local Similarity 68.9%; Pred. No. 7.4e-111;
Matches 272; Conservative 72; Mismatches 50; Indels 1; Gaps 1;

QY 90 PYATGPASHISPRAWRRPTTISHHVAISDAEDCVOLNQYKLGSEIGKGYVVRLAYNES 149
DB 11 PYSPVSSQSSPRLPRPTVSHHVSITGMQDCVOLNQYTLKDEIGKGSYGVVKLAYNEN 70
QY 150 EDHYAMKVLKSKKLLKQYGFPRPPRPGSQAAQGGPAKQLLPLERVVYOEIATLKKLDHV 209
DB 71 DNTYAMKVLKSKKLLKQYGFPRPPRPGSQAAQGGPAKQLLPLERVVYOEIATLKKLDHV 130
QY 210 NVVKLIEVLDPAEDNLYLVFDLRLKGPVMEVPCDKPFSEEQARLYLRDVLGLGYLHCQ 269
DB 131 NVVKLIEVLDPAEDNLYLVFDLRLKGPVMEVPCDKPFSEEQARLYLRDVLGLGYLHCQ 190
QY 270 KIVHRDIKPSNLLIGDDGHVKIADFGVSNQEPGNDALSSTAGTPAFMAPEAISQSGSF 329
DB 191 KIIHRDIKPSNLLIGDDGHVKIADFGVSNQEPGNDALSSTAGTPAFMAPEAISQSGSF 250
QY 330 SGKALDVMATGTYLCFYVYKCPFDIDDFILALHRRKIKNEPVVFPPEPEI SEELKDLILKM 389
DB 251 SGKALDVMATGTYLCFYVYKCPFDIDDFILALHRRKIKNEPVVFPPEPEI SEELKDLILKM 310
QY 390 LDKNPETRIGVDPDKLHPWTKNGEELPLPSSEHCVSVVVTEGVKNSVRIPSWTTVIL 449
DB 311 LDKNPESRIVVPEIKLHPWTRHGAELPLPSDENCTLVEVTEEVENSVKHIPSATVIL 370
QY 450 VKSMRLKESFGNPPEQARRREERSMSAPGNLLVKE 484
DB 371 VKTMIRKRSFGNPPE-GSRREERSLSAPGNLLTKK 404
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Search completed: July 12, 2004, 05:55:51
Job time : 1697 secs
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